CDA-1 Galskum

us-09-635-974a-2.rag

	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - pr	OM protein - protein search, using sw model
Run on:	October 6, 2004, 16:20:48 ; Search time 25.2632 Seconds (without alignments) 55.921 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-635-974A-2 31 1 NYGVH 5
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	1586107 segs, 282547505 residues

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 29Jan04:* 1: geneseqp1980s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aaw08938 CDR1 from	Aay59311 Heavy cha	ď	Aau77784 Mouse hea	Abo32615 Secreted	9	m	Aag33864 Arabidops	m	Aaw08950 Heavy cha	Aaw08952 Heavy cha	Aaw08951 Heavy cha		Aay90818 260F9 hyb	Human	Aaw08947 Heavy cha	Aaw08944 Heavy cha		Aay79257 Putative	Aau00478 Rat INTER	Abo32630 Secreted	Aay79267 Mouse put	7 Murine	Abo32622 Secreted	Aae37329 Human VLC
ID	AAW08938	AAY59311	AAB37952	AAU77784	AB032615	AAM93396	AAW05823	AAG33864	AAW08953	AAW08950	AAW08952	AAW08951	AAW08954	AAY90818	AAB00210	AAW08947	AAW08944	AAW08942	AAY79257	AAU00478	AB032630	AAY79267	AAU00477	AB032622	AAE37329
DB	7	m	4	Ŋ	ø	4	7	ო	N	~	7	Ŋ	N	m	m	N	N	~	m	4	ų	m	4,	ω	9
Length	ß	S	ហ	Ŋ	19	107	116	117	119	119	119	119	119	119	130	138	138	138	141	144	144	147	174	174	179
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	31	31	37	31	31	7 31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
Result No.	н	α	m	4	2	9	7	œ	σn	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aaw29676 Homo sapi Abo32609 Secreted Aar43679 Single ch	Aar99649 Single ch Aaw02191 18-2-3/TR Aaw02133 Single ch Sam03344 Human nol	18-2- 18-2- Singl		Aay79266 Human elo Aab29648 Human mem Aau00476 Human INT	Aau87832 Human elo Aae24555 Human ELG Aag79838 ADSL rela Ab032607 Secreted
2 AAW29676 5 ABO32609 8 AAR43679	AAR99649 AAW02191 AAW05133	AAR06482 AAR06483 AAR43680	AAR99650 AAW02192 ABP44994	AAY79266 AAB29648 AAU00476	AAU87832 AAE24555 AAG79838 ABO32607
211 219 239 2	2239	2444 2444 2422	242 242 251 5	265 265 3 265 4	2 2 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
31 100.0 31 100.0 31 100.0	31 100.0 31 100.0	31 100.0	31 100.0 31 100.0 31 100.0	31 100.0 31 100.0 31 100.0	31 100.0 31 100.0 31 100.0 31 100.0
26 27 28	2 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9) W W W 1 W 4. N	36 37 38	8 4 4 0 0 11	4 4 4 4 ሪ 6 4 7

ALIGNMENTS

RESULT 1

Complementarity determining region 1; CDR1; heavy chain; variable region; reshaped; human; monoclonal; antibody; H225; epidermal growth factor; BGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate. - nseq Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour. CDR1 from heavy chain variable region of reshaped H225 antibody. Goldstein NI, Giorgio NA, Jones ST, Saldanha JW; Ä. (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT. AAW08938 standard; peptide; 5 96WO-US009847. 95US-00482982. 95US-00573289. 18-SEP-1997 (first entry) WPI; 1997-051897/05. WO9640210-A1. Homo sapiens. 07-JUN-1995; 15-DEC-1995; 07-JUN-1996; 19-DEC-1996. AAW08938; AAW08938

The present peptide is the complementarity determining region 1 (CDR1) from the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, which is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour calls, especially late stage prostatic tumour cells in humans, optionally conjugated a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell Claim 1; Page 83; 112pp; English.

Sequence 5 AA;

cycle inhibitor

```
AAB37952 standard; protein; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the hypervariable region CDRI (complementarity determining region 1) of the heavy chain of a single chain antibody derived from the murine antibody 225. The invention relates to a method for inhibiting the growth of tumours in human patients by treating with an effective amount of a combination of radiation and a non-radiolabelled protein receptor tyrosine kinase (PRTK) inhibitor, the overexpression of which can lead to tumourigenesis. The method can be used in the treatment of tumours of e.g. breast, lung, colon, kidney, bladder, head and neck, ovary, prostate or brain. The administration of a suitable antibody to the patient makes the tumour more susceptible to radiotherapy
                                                                                                                                                                                                                 Hypervariable region; complementarity determining region; CDR; tumour; single chain antibody; growth inhibitor; human; tumourigenesis; therapy; protein receptor tyrosine kinase; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of human tumors, using a combination of radiation and a non-radiolabeled protein receptor tyrosine kinase inhibitor.
                                 Gaps
                                 .
0
           Length 5;
          / Match 100.0%; Score 31; DB 2; Length 5; Local Similarity 100.0%; Pred. No. 1.4e+06; nes 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 31; DB 3; I
100.0%; Pred. No. 1.4e+06;
ive 0, Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          Buchsbaum DJ;
                                                                                                                                                                                             Heavy chain hypervariable region, CDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 14; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          Robert F,
                                                                                                                             AAY59311 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                              98US-00079612.
98US-0085613P.
98US-00206138.
                                                                                                                                                                                                                                                                                                                           99WO-US010741.
                                                                                                                                                                                                                                                                                                                                                                                        (IMCL-) IMCLONE SYSTEMS INC. (UABR-) UAB RES FOUND.
                                                                                                                                                                       07-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity luv.
                                                                                                                                                                                                                                                                                                                                                                                                                          Saleh MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-062440/05.
                                                     2
                                                                           Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ48625
                                                                       NYGVH
                                                     NYGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                              15-MAY-1998;
15-MAY-1998;
07-DEC-1998;
                                                                                                                                                                                                                                                                                  WO9960023-A1
                                                                                                                                                                                                                                                                                                                           14-MAY-1999;
                                                                                                                                                                                                                                                                                                      25-NOV-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                          Waksal HW,
                                                                                                                                                    AAY59311;
             Query Match
                                                                                                                                                                                                                                                             Mus sp.
                         Best Loc
Matches
                                                                                                                   임
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a method for inhibiting the growth of factor receptor (EGFR) in human parients. The method involves treating the patient with a combination of EGFR/human EGF-1 (HER1) antegonist, optionally with a chemotherapeutic agent or radiation. The antagonist can be for example a chimeric anti-EGFR monoclonal antibody, C255. The EGFR/HER1 antagonist is useful for inhibiting the growth of refractory tumours such as tumours of breast, heart, lung, small intestine, colon, spleen, kidney, bladder, head and neck, ovary prostate, brain, pancreas, skin, bone, bone marrow, blood, thymus, uterus, testicles, cervix and liver, preferably squamous cell carcinomas. The present sequence represents the heavy chain variable region complementarity determining region 1 amino acid sequence of the chimeric anti-EGFR monoclonal antibody C225 which is used in an example illustrating the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Epidermal growth factor receptor/human epidermal growth factor receptor-1 antagonist for inhibiting the growth of refractory tumors.
                                                                                                            Refractory tumour growth inhibition; epidermal growth factor receptor; BGFR antagonist; cancer; squamous cell carcinoma; anti-EGFR antibody; complementarity determining region; CDR.
                                                    Anti-EGFR monoclonal antibody H chain V region CDR1 peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse heavy chain hypervariable region (CDR1) of 225 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; heavy chain; antibody; hyperproliferative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 13; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU77784 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00312284.
                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000; 2000WO-US011756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMCL-) IMCLONE SYSTEMS INC
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-016160/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC83235
                                                                                                                                                                                                                                                                                            WO200069459-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NYGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1999;
13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-2002
12-MAR-2001
                                                                                                                                                                                                                                                                                                                                                   23-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waksal HW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU77784;
                                                                                                                                                                                                                                    ds sny
```

Gaps

;

0; Indels

.;

1 NYGVH 5

NYGVH 5

g

RESULT 3 AAB37952

US2003022279-A1.

30-JAN-2003

```
RESULT 6
  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                     of a member of the EGF receptor family, or a combination of the antiagonist and photocherapy, chemotherapeutic agent or radiation therapy. The antibody used in the method of the invention acts as an epidermal growth factor receptor (EGFR) antagonist by inhibiting EGFR /HERI phosphorylation. The method of the invention is useful for traating a mammal with hyperproliferative disease such as psoriasis, actinic keratoses, seborrheic keratoses, warts, keloid scars and cacama signilated by a ligand of a member of the EGF family of receptor. This sequence represents the murine anti-EGF 255 antibody heavy chain (VH) hypervariable region (CDR1) used as an inhibitor of EGFR in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, TANGO, INTERCEPT, secreted polypeptide; immune disorder;
hormonal disorder; proliferative disorder; cancer; thyroid disorder;
diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
myocardial infarction; congestive heart disease; blood platelet disorder;
thrombocytopenia; blood vessel; atherosclerosis; vasculitis.
                                                                                                                                                                                                                                                             Treating a mammal with hyperproliferative disease especially psoriasis, stimulated by ligand of member of epidermal growth factor family of receptors, by administering antagonist of the receptor.
                                                                                                                                                                                                                                                                                                                                       This invention relates to a novel method for treating a mammal with hyperproliferative disease stimulated by a ligand of a member of the epidermal growth factor (BGF) family of receptors. The method involves administering an antibody or a defective receptor that is an antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
epidermal growth factor; EGF; psoriasis; actinic keratosis; seborrheic keratosis; warts; keloid scars; eczema; 255 antibody; hypervariable region; CDR1; EGFR inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 31; DB 5; Length 5; 100.0%; Pred. No. 1.4e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted polypeptide-related peptide #42.
                                                                                                                                                                                                                                                                                                                Disclosure; Page 11; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO32615 standard; peptide; 19 AA.
                                                                                                                                                   09-AUG-2000; 2000US-00635974.
                                                                                                                          09-AUG-2001; 2001WO-US041647.
                                                                                                                                                                          (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                         WPI; 2002-257423/30.
N-PSDB; ABK11440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYGVH 5
                                                                         WO200211677-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5 AA;
                                                                                                  14-FEB-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-2003
                                                                                                                                                                                                   Teufel T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABO32615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                   Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
ABO32615
 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
The invention relates to secreted polypeptide-related proteins and nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The nucleic acids, proteins and antibodies specific to the proteins are uncleic acids, proteins and antibodies specific to the proteins are useful in screening assays, predictive medicine (e.g. diagnostic assays, prognostic assays monitoring clinical trials and pharmacogenetics) and thorapeutic methods. The sequences are used in classification problems proliferative disorders (e.g. andithiple sclerosis or lupus), neurological disorders (e.g. multiple) sclerosis or lupus), neurological disorders (e.g. disorders (e.g. multiple) sclerosis or lupus), neurological disorders (e.g. propolated electrosis or lupus), neurological disorders (e.g. thrombotycopenia or anaemia) and disorders cinvolving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic acids may also be used in chromosome mapping, tissue typing and forensic polypeptide-related peptide of the invention. Note: The sequence data for this patent was obtained in electronic format directly from USPTO at sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202, TANGO 201, TANGO 201 or INTERCEPT 217), useful for diagnosing, preventing or treating disorders such as cancer, diabetes or atherosclerosis, and in forensic biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
Mccarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 31; DB
100.0%; Pred. No. 17;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; SEQ ID NO 231; 482pp; English.
                                                                               99US-00342364.
99US-00393996.
99US-00420707.
                                                                                                                                                           2000US-00479249.
2000US-00559497.
2000US-00578063.
                                                                                                                                                                                                                                       16-JUN-2000; 2000US-00596194.
23-JUN-2000; 2000US-00602871.
30-JUN-2000; 2000US-00608452.
12-JAN-2001; 2001US-00759130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MACKAY C R.
GOODEARL A D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barnes TM,
                                                                                                                                                                                                                                                                                                                                            FRASER C C.
BARNES T M.
SHARP J D.
KIRST B J.
MYERS P S.
LEIBY K R.
HOLIZMAN D A.
WRIGHTON N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-456290/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 AA;
                                                                                                                                                           07-JAN-2000; 27-APR-2000; 24-MAY-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DA,
                                                                            29-JUN-1999;
10-SEP-1999;
19-OCT-1999;
                                                     14-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holtzman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HOLT/) 1 (MCCA/) 1 (WRIG/) 1 (MACK/) 1 (GOOD/)
                                                                                                                                                                                                                                                                                                                                               (FRAS/)
(BARN/)
                                                                                                                                                                                                                                                                                                                                                                                                  (SHAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                              (KIRS/)
(MYER/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LEIB/)
```

ö

NYGVH 10

φ

```
Homo, sapiens.
Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                            29-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                     WO9626964-A1
                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-1996,
                    Chimeric.
                                                                                                                                                                                          Region
                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                         Region
ö
                                                                                                                                                                                                                                                                                                                                               The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                                                                                                                                                   830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                   Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B-cell lymphoma; humanised antibody; bispecific antibody; myeloma; leukaemia; hybridoma; monoclonal antibody.
                                                                                                                                                                                                                                        Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID NO 2992; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 31; DB 4; Length 107; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                              Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised 1D10 antibody heavy chain variable region.
                                                         Human polypeptide, SEQ ID NO: 2992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW05823 standard; protein; 116 AA.
AAM93396 standard; protein; 107 AA
                                                                                                                                                                                       11-JAN-2000; 2000JP-00118774.
                                                                                                                                                           07-JUL-2000; 2000EP-00114089.
                                                                                                                                                                               99JP-00194486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                              in genetic manipulation.
                                                                                                                                                                                                                      (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2003 (revised)
27-JAN-1997 (first en
                                                                                                                                                                                                                                                                      WPI; 2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYGVH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NYGVH 5
                                                                                                                                                                                                                                                                                 N-PSDB; AAK94317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 107 AA;
                                                                                                                                                                              08-JUL-1999;
                                                                                                 Homo sapiens
                                                                                                                    EP1130094-A2
                                      06-NOV-2001
                                                                                                                                        05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW05823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                   AAM93396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW05823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
```

```
The variable region (AAMO5823) of the humanised IDIO antibody heavy chain (AAMO5829) consists of human IC4 heavy chain variable region framework (substd. at 9 positions with mouse or consensus human amino acids) and complementarity determining regions from the murine IDIO antibody specific for a 28/32 kDa heterodimeric antigen present on the surface of malignant B-cells. It can be coexpressed with humanised IDIO light chain (see also AAWO5828) in e.g. mouse myelome NSO cells. Humanised antibody fragments can be incorporated into novel bispecific antibodies reactive Walth both effector cell antigens (see also AAWO5820) and malignant B-cells. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New bi-specific antibody reactive with both T or NK cells and malignant foels - also their humanised forms and hybridomas producing them, useful for treating or preventing leukaemia, lymphoma and myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "human framework residue 82 is substd. by a consensus amino acid of the equivalent murine framework residue"
                 /note= "human framework residue 27 is substd. by
equivalent murine framework residue"
29
                                                                                                                                      þ
                                                                                                                                                                                                                       ρχ
                                                                                                                                                                                                                                                                                                                                                        ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ρχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ģ
                                                                                              /note= "human framework residue 29 is substd.
equivalent murine framework residue"
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "human framework residue 71 is substd.
equivalent murine framework residue"
Misc-difference 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "human framewoek residue 73 is substd.
equivalent murine framework residue"
Misc-difference 78
                                                                                                                                                                                                                 /note= "human framework residue 30 is substd. equivalent murine framework residue"
                                                                                                                                                                                                                                                                                                                                            /note= "human framework residue 37 is substd.
equivalent murine framework residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "human framework residue 68 is substd.
equivalent murine framework residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "human framework residue 78 is substd. equivalent murine framework residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tso JY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROT-) PROTEIN DESIGN LABS INC.
(IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Link BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Fig 4b; 85pp; English.
                                                                                                                                                                                                                                                                          31. .35
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                              50. .65
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98. .105
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US002754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-00397411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weiner G, Gingrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-412742/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 67
                               Misc-difference
                                                                                                               Misc-difference
                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                              Misc-difference
```

```
99045 - 0138840 P 9905 - 01388410 P 9905 - 0139452 P 9905 - 0139452 P 9905 - 0139455 P 9905 - 014295 P 9905 - 0144333 P 9905 - 014598 P 9905 - 0145919 P 9905 - 0145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 - 70L - 1999
22 - 70L - 1999
23 - 70L - 1999
23 - 70L - 1999
24 - 70L - 1999
25 - 70L - 1999
27 - 70L - 1999
27 - 70L - 1999
27 - 70L - 1999
28 - 70L - 1999
28 - 70L - 1999
29 - 70L - 1999
20 - 70L - 199
   ö
                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                          Gaps
                                                                        ..
                                    Length 116;
                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 41114.
                                    Query Match 100.0%; Score 31; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                       AAG33864 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9905-0121825P

9905-0123180P

9905-0125788P

9905-01264P

9905-01264P

9905-01264BP

9905-01264BP

9905-0128234P

9905-0128234P

9905-0128234P

9905-013891P

9905-013891P

9905-0130891P

9905-0130891P

9905-0132484P

9905-0132484P

9905-0132484P

9905-0132484P

9905-0132484P

9905-0132484P

9905-0132484P

9905-0132484P

9905-013421P

9905-013422P

9905-013422P

9905-013422P

9905-013422P

9905-013422P

9905-013422P

9905-013422P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000EP-00301439
                                                                                                                                                                                                                                                                                                            18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                       31 NYGVH 35
                                                                                                           1 NYGVH 5
   Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FBB-1999;
05-MAR-11999;
23-MAR-11999;
25-MAR-11999;
25-MAR-11999;
06-APR-11999;
06-APR-11999;
10-APR-11999;
10-APR-11999;
23-APR-11999;
30-APR-11999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000
                                                                                                                                                                                                                                                                         AAG33864;
                                                                                                                                                                                                   RESULT 8
AAG33864
   g
                                                                                                                                                                                                                                                        8
```

φ

```
Heavy chain; reshaped; monoclonal; antibody; 225RD; human; eppldermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saldanha JW;
                                                                                                                                                                                     Heavy chain variable region of 225RD antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                          109. .119 __/label= framework_4
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                             AAW08953 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 30; Fig 22; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US009847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-00482982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98. .108
/label= C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-051897/05.
 |||||
NYGVH 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 119 AA;
                                                                                                                                                         18-SEP-1997
                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-1996
                                                                                                                         AAW08953;
                   21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                             HINDER STATE TO THE STATE OF THE STATE TO THE STATE OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 31; DB 3; Length 117; ilarity 100.0%; Pred. No. 1.2e+02; Conservative 0; Mismatches 0; Indels
99US-0147935P.
99US-0148111P.
99US-0148311P.
99US-0148565P.
99US-0148565P.
99US-0149368P.
99US-0149722P.
99US-0149723P.
99US-0149723P.
99US-0149723P.
99US-0149723P.
99US-0159723P.
99US-0150884P.
99US-0150884P.
99US-0150884P.
99US-0150884P.
99US-0150884P.
99US-0150884P.
99US-0150884P.
99US-0150884P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   99US - 0155139P.
99US - 0155486P.
99US - 0155659P.
99US - 0156596P.
99US - 0157117P.
99US - 015731P.
99US - 0157659P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0158369P.
99US-0159293P.
99US-0159294P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0159295P.
99US-0159329P.
99US-0159330P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9905-0159638P
9905-0159584P
9905-016074P
9905-0160768P
9905-016070P
9905-016091P
9905-016080P
9905-016080P
9905-0160980P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0161359P.
99US-0161360P.
99US-0161361P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0161404P.
99US-0161405P.
99US-0161406P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0161992P.
99US-0161993P.
99US-0162142P.
                                                                                                                                                                                                                                                                                                                                                                                          99US-0154018P
                                                                                                                                                                                                                                                                                                                                                                                                       99US-0154039P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0158232P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0159331P.
99US-0159637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0161920P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                       20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                         13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                 27-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-1999
```

·. The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) #225, 225RHD. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells, especially late stage agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor Gaps ·. Similarity 100.0%; Score 31; DB 2; Length 119; Similarity 100.0%; Pred. No. 1.2e+02; 5; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 5; Conser

1 NYGVH 5

8

1 NYGVH 5

δ

ö

Gaps

```
NYGVH 35
                                                                           18-SEP-1997
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                WO9640210-A1
                                                                                                                                                                                                                                                                                                                                07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                                                                                19-DEC-1996.
                                                           AAW08952;
    31
                                           AAW08952
                                                                                                                                                                  Key
Region
                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                         Region
                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                          Region
                                    AAW08952
                                                  The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H255, 225RH. The MAD is specific for the human monoclonal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage agent tumour calls in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                         Heavy chain; reshaped; monoclonal; antibody; 225RA; human; eppidermal growth factor; RGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostatic; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                               - used
                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                               Saldanha JW;
                                                                                        Heavy chain variable region of 225RA antibody.
                                                                                                                                                                                                                                                                                                                                                                                             Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                      36. .49
/label= framework_2
50. .65
/label= CDR_2
66. .97
/label= framework_3
                                                                                                                                                                                                                                                                      Æ.
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                         .30
label= framework_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 30; Fig 22; 112pp; English.
                                         AAW08950 standard; protein; 119
                                                                                                                                                                                                                                                                                                                                                                     (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                CDR_1
                                                                                                                                                                                                                                                        98. .108
/label=_CDR_3
                                                                                                                                                                                                                                                                                                                                              95US-00482982.
95US-00573289.
                                                                                                                                                                                                                                                                                                                              96WO-US009847
                                                                         (first entry)
                                                                                                                                                                                                                                                       108
                                                                                                                                                                                        31. .35
/label= (
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-051897/05.
31 NYGVH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                              07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
15-DEC-1995;
                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                               WO9640210-A1
                                                                         18-SEP-1997
                                                                                                                                                                                                                                                                                                               19-DEC-1996
                                                         AAW08950;
                                                                                                                                                                 Key
Region
                                                                                                                                                                                        Region
                                                                                                                                                                                                        Region
                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                        Region
                                   AAW08950
```

```
ö
                                                                                                                                                                                                           Heavy chain; reshaped; monoclonal; antibody; 225RC; human; eppidermal growth factor; EGF, receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the heavy chain variable region of the reshaped human monoclonal attribody (MAb) H225, 225RHC. The MAb is specific for the human epidermal growth factor (EEF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 31; DB 2; Length 119; ilarity 100.0%; Pred. No. 1.2e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saldanha JW;
                                                                                                                                                          Heavy chain variable region of 225RC antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                  11.30

/label= framework_1

31..35

/label= CDR_1

36..49

/label= framework_2

/label= CDR_2

/label= CDR_2

/label= CDR_2
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 30; Fig 22; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98. .108
/label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-00482982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US009847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
```

Gaps

;

Indels

100.0%; Score 31; DB 2; Length 119; llarity 100.0%; Pred. No. 1.2e+02; Conservative 0; Mismatches 0; Indels

Best_Local Similarity
Matches 5; Conserv

Query Match

tumour; cell;

```
Heavy chain; reshaped; monoclonal; antibody; 225RE; human; apidermal growth factor; EGF; receptor; inhibition; growth; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                   Heavy chain variable region of 225RE antibody.
                                                          AAW08954 standard; protein; 119 AA.
                                                                                                 (first entry)
31 NYGVH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 119 AA;
                                                                                                 18-SEP-1997
                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                        WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-1996
                                                                              AAW08954;
                                                                                                                                                                                                             Key
Region
                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                           Region
                                        RESULT 13
                                                 AAW08954
                                                                     Heavy chain; reshaped; monoclonal; antibody; 225RB; human; epidermal growth factor; BGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H255, 225RHB. The MAD is specific for the human monoclonal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage spotsatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or displatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 31; DB 2; Length 119; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saldanha JW;
                                                                                                                     Heavy chain variable region of 225RB antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                            36. .49
/label= framework_2
50. .65
/label= CDR_2
                                                                                                                                                                                                                                                                                                    66. .97
/label= framework_3
                                                                                                                                                                                                                                                                                                                                          109. .119 ___/label= framework_4
                                                                                                                                                                                                                        .. .30
/label= framework_1
                                                                                                                                                                                                            Location/Qualifiers
                                                            AAW08951 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 30; Fig 22; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                 CDR_3
                                                                                                                                                                                                                                           31. .35
/label= CDR_1
                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US009847
                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00482982.
                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-00573289,
                                                                                                  18-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                      98. .108
/label= CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-051897/05.
31 NYGVH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 119 AA;
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                         WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1996.
                                                                               AAW08951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                              Key
Region
                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                             Region
                                                AAW08951
ID AAW
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAb) H225, 225RHE. The MAb is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells, especially conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 31; DB 2; L
100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goldstein NI, Giorgio NA, Jones ST,
                                                                                                  346..49
/label= framework_2
50..65
1..65
66..97
/label= framework_3
                                                                                                                                                                                                                                                                         . .30
label= framework_1
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 30; Fig 22; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                    CDR_1
                                                                                                                                                                                                                                                       CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00482982.
                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US009847
                                                                                                                                                                                                                                   .108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                              31. .35
/label=
                                                                                                                                                                                                                                                     label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

ö

Gaps . 0

5; Conservative

Best Local Similarity

Matches

```
The present invention describes a monoclonal antibody (MAD) (I) that binds to a human breast cancer antigen that is also bound by MAD 454C11 and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also described is a hybridoma that produces (I). (I) is useful in specific binding assays, affinity purification, drug or toxin targeting, imaging, and genetic or immunological therapeutics for various cancers. The present sequence represents a VH domain derived from a 260F9 hybridoma, which is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody capable of binding to human breast cancer antigen useful for affinity purification, drug or toxin targeting, imaging, and
                                                                                                                    Antigen binding site; immunoglobulin; cancer antigen; immunological; antibody; tumour; human; mucin; cancer; cytostatic; hybridoma; specific binding assay; affinity purification; drug targeting; toxin targeting; imaging; genetic; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 31; DB 3; Length 119; 100.0%; Pred. No. 1.2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                         260F9 hybridoma VL domain SEQ ID NO:14.
AAY90818 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB00210 standard; protein; 130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 7; 57pp; English.
                                                                                                                                                                                                                                                                                                                   84US-00577976.
85US-00690750.
86US-00842476.
88US-00190778.
94US-00288981.
                                                                                                                                                                                                                                                                                           95US-00483749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-338508/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 NYGVH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA38902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON
                                                                                                                                                                                                                                                                                                                                     11-JAN-1985;
21-MAR-1986;
08-MAY-1988;
11-AUG-1994;
                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                        07-JUN-1995;
                                                            29-AUG-2000
                                                                                                                                                                                                                              US6054561-A.
                                                                                                                                                                                                                                                            25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-2001
                                AAY90818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB00210
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ring DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB00210
                                ઠે
```

Gaps

.. 0

..

5; Conservative

6, 2004, 16:29:42

completed: October le : 29.2632 secs

Search cor Job time

ö

ò d

Length 130; 0; Indels

```
New elongase polypeptides which are functional long chain polyunsaturated fatty acid (PURA) elongase polypeptides are described. The elongase catalyses an elongase reaction to produce PURA (24 carbon fatty acid with at least 4 double bonds) such as di-homo-gamma-linoleic acid (20:3Delta8,11,14), arachidonic acid (20:4Delta5,8,11,14), elocosapentanoic acid (20:5Delta8,11,14), docosatetraenoic acid (22:3Delta3,16,19), docosatetraenoic acid (22:4Delta7,10,13,16,19), bufA produced is useful in foodsutffs, dieta7y supplements and in pharmaceutical compositions which can then be used to elavate PURA levels of an animal or plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated polypeptide comprising functional long chain polyunsaturated fatty acid (PUFA) elongase of Caenorhabditis elegans used to produce PUFA for foodstuff, dietary supplement or pharmaceutical
                                                                                                            Elongase; polyunsaturated fatty acid; PUFA; dietary supplement; pharmaceutical; foodstuff; food; di-homo-gamma-linoleic acid; arachidonic acid; elcosapentanoic acid; docosatrienoic acid; docosatetraenoic acid; docosapentaenoic acid; docosabentaenoic ac
                                    Human sequence (BAC207d4) related to PUFA elongase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 31; DB 3; I
100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 10; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99GB-00006307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-2000; 2000WO-GB001035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYBR-) UNIV BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-647074/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       WO200055330-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1999;
18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Napier JA;
                                                                                                                                                                                                                                                                          human.
```

This Page Blank (uspto)

P74540 synechocyst Q9ma74 arabidopsis Q9sm21 brassica na Q9gyb6 leishmania Q8dgal synechococc gagas burkholderi Q8hako burkholderi Q8hako burkholderi Q8hako burkholderi Q8hako burkholderi Q86nja caenorhabdi Q9ggq caenorhabdi Q9aqq drosophila Q7agg haliotis di Q9vgq drosophila Q7agg haliotis di Q9vgq drosophila Q7agg haliotis di Q9vgq drosophila Q7agg shoococ Q8yils methanosarc Q8lis methanosarc

P74540 99XA74 Q9XXA74 Q9XXI2 Q9GXB6 Q8BGA1 Q8BB62 Q8BB62 Q8BB62 Q8BB62 Q8CGA4 Q9CGA4 Q9CGA9 Q9CGA9 Q9CA105 Q9CA105 Q9TA05 Q9TA05 Q9TA07 Q8TA01 Q8TA11 Q8TA11

10

```
PRELIMINARY;
444825
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
6620
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
66220
                                                                                                                                                                                                                               1000.0
1000.0
1000.0
996.8
996.8
996.8
996.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8NCD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
Q8NCD1
Q8ncd1 homo sapien
Q8rep9 homo sapien
Q8rmi3 anabaena ep
Q9h5j4 homo sapien
Q92016 fattus norv
Q8ce45 mus musculu
Q92015 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09xx22 caenorhabdi
093x22 caenorhabdi
09bv4 homo sapien
09c30 homo sapien
09c19 homo sapien
09h076 homo sapien
09h076 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                            October 6, 2004, 16:23:13; Search time 16.7544 Seconds (without alignments) 94.160 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                          1017041
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                           1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8TEP9
Q8YM13
Q9YM13
Q942014
Q92015
Q92015
Q931Z9
Q931Z9
Q931Z9
Q98C30
Q96C30
                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_archeap:*
                                                                                                                                                       US-09-635-974A-2
31
1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                          SPTREMBL 25:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                           Searched:
                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
No.
```

ö LIUNCE FROM N.A.

SEQUENCE FROM N.A.

I SEQUENCE FROM N.A.

I SEQUENCE T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,

A Suzuki Y., Nagai K., Sugano S., Ishii S., Kawal-Hio Y., Salto K.,

Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,

A Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

"NEDO human CDNA sequencing project.", Ninomiya K.;

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

SMBL, AXOT4813; BAC11-25-1,
R GO; GO:0016021; C:integral to membrane; IEA.

InterPro; IPR002076; GNS1_SUR4.

InterPro; IPR0115; ELO; 1.

R PROSTITE; PS01168; ELO; 1.

W Hypothetical protein.

SEQUENCE 240 AA; 28271 MW; 38A101DCF141818E CRC64; Gaps Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. . 0 100.0%; Score 31; DB 4; Length 240; 100.0%; Pred. No. 61; 0; Indels tive 0; Mismatches 0; Indels 01-0CT-2002 (TrEMBLrel. 22, Created) 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-1UN-2003 (TrEMBLrel. 24, Last annotation update) Hypothetical protein FLJ90332. Homo sapiens (Human). PRT; Query Match
Best Local Similarity 100.v 145 NYGVH 149 1 NYGVH 5 g

O9dbs1 mus musculu O8pkv6 xanthomonas O8ebw6 shewanella

```
Query Match
Best Local Similarity 100...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 NYGVH 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q920L6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT :
       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | SEQUENCE FROM N.A. | Sasamoto S., | MEDLINE=21595285; PubMed=11759840; | MEDLINE=21595285; PubMed=11759840; | Marita T., Sasamoto S., | MEDLINE=21595285; PubMed=11759840; | Marita T., | Nakamura Y., | Wolk C.P., | Kuritz T., | Kamura T., | Kanida Y., | Kohara M., | Matsumoto M., | Matsumo A., | Muraki A., | Makazaki N., | Shimpo S., | Sugimoto M., | Takazawa M., | Yamada M., | Yasuda M., | Tabata S.; | Sugimoto M., | Takazawa M., | Yamada M., | Yamada M., | Yamada M., | Yasuda M., | Yamada M., | Yamada M., | Yasuda M.
                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Spleen;
Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
"The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 31; DB 16; Length 263; 100.0%; Pred. No. 67; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 31; DB 4; Length 255; 100.0%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spleen.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AK074073; BAB84899.1;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 255 AA; 28454 MW; BF85941BB2012999 CRC64;
                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
FLJ00144 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein All4950.
                                           255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 AA
                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.00
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.

10s 5; Conservative
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 NYGVH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 NYGVH 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NYGVH 5
                                                                                                                                                                                                                                                                       FLJ00144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8YMI3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALL4950
                                           Q8TEP9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8YMI3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
Q9H5J4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
OGYMAN
AC OGYM
DT 01-M
DT 01-V
DT 01-
OS TEP 9 OS 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

PRELIMINARY;

Q9H5J4 Q9H5J4;

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                     SEGUENCE FROM N.A.

Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification and expression of a mammalian fatty acid elongase involved in de novo biosynthesis of C18 fatty acids."; bubmitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, ABO71986; BAB66988.1; -...

GO, GO:0016021; C:integral to membrane; IEA.

InterPro; PR002776; GNS1_SUR4.

Pfam; PF01151; ELO; 1.

PROSITE; PS01188; ELO; 1.

SEQUENCE 267 AA; 31624 MW; 4026C9CB33ED0743 CRC64;
                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 31; DB 11; Length 267; 100.0%; Pred. No. 68; 0; Indels ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Sprague Dawley, TISSUB-Liver;
Inagaki K., Aki T., Fukuda Y., Kawamoto S., Shigeta S., Ono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 31; DB 4; Length 265; 100.0%; Pred. No. 67; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027031; BAB15632.1; -.
EMBL; BC001305; AAH01305.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:15829; ELOVLG.
GO:0016021; C:integral to membrane; IEA.
InterPro; IPR002076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
PROSTITE; PS01188; ELO; 1.
PROSTITE; PS01188; ELO; 1.
SEQUENCE 265 AA; 31376 MW; 01234E0EEF6CE341 CRC64;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                          Hypothetical protein FLJ23378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fatty acid elongase 2.
```

```
1)

SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-Skin;

STRAIN-C57BL/6J; TISSUE-Skin;

X MEDLINE-22354683; PubMed-12466851;

A The FANTOM CONSORTIUM,

the RIKEN Genome Exploration Research Group Phase I & II Team;

Analysis of the mouse transcriptome based on functional annotation of the North Call-Inengh CDNAs.";

A Manure 420:563-573 (2002)

N MGT: 2165629; Barca6221;

N MGT: 2165628; Blov46.

R MGD: MGT: 2165628; Blov46.

R MGD: MGT: 2165628; Blov46.

R MGD: MGT: 2165629; Blov46.

R MGD: MGT: 2166629; Blov46.

R MGG: MGG: 2166429; Blov46.

R MGG: MGG: 2166429; Blov46.

R MGG: MGG: 2166429; Blov46.

R MGG: 2166429; Blov46.

R MGG: MGG: 2166429; Blov46.

R MGG: 2166429; Blov469.

R M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fatty acyl elongase (Long-chain fatty-acyl elongase) (Myelination associated SUR4-like protein).
BLOVIG OR FAE OR LCE OR MASR.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mummalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=21576178; PubMed=11567032;
Moon Y.A., Shah N.A., Mohapatra S., Warrington J.A., Horton J.D.;
Identification of a Mammalian Long Chain Fatty Acyl Elongase
Regulated by Sterol Regulatory Element-binding Proteins.";
J. Biol. Chem. 276:45358-45366 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

TRAINA-CS7816, TISSUB-Liver;

Matsuzaka T., Shimano H.;

"murine complete cds for new fatty acyl elongase similar to cig30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 31; DB 11; Length 267; 100.0%; Pred. No. 68; 0; Indels ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01151, BLO, 1.
SEOUENCE 267 AA; 31601 MW; 4031F9C503E4DD23 CRC64;
                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Long chain fatty acyl elongase.
ELOVIG OR LCE.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 AA.
                                                                                                                                                                                                               267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 NYGVH 174
170 NYGVH 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q920L5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0920L5
                                                                                                                               RESULT 6
                                                                                                                                                                              08CE45
                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPART REPARENT REPAR
```

```
Strausberg R.;
Submitted (A.P. 2013) to the EMBL/GenBank/DDBJ databases.

EMBL; AB072039; BAB6844.1; -.

EMBL; A8053453; AAL14239.1; -.

EMBL; A80560; AAM13450.1; -.

EMBL; AV651041; AAH51041.1; -.

MCD; MCJ:2156528; Elov16.

GO; GO:001767; F:transferase activity, transferring groups o. .; IDA.

GO; GO:0030497; P:transferase activity, transferring groups o. .; IDA.

GO; GO:001574; P:transferase activity, transferring groups o. .; IDA.

InterPro; IPR002076; GNS1_SUR4.

FEAM; PRO1151; ELO; 1.

PROSITE; PS01188; ELO; 1.

SEQUENCE 267 AA; 31610 MW; 4026C9CB33FDDD23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       investigating biology.";

Science 282:2012-2018(1998).

Science 282:2012-2018(1998).

1. SUBCELULIAR LOCATION: NUCLEAR (BY SIMILARITY).

1. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

BMBL; AL031632; CAA21008.1; -.

BMBL; AL031632; CAA21008.1; -.

BMBL; AL031632; CAA21008.1; -.

BMBL; AL031632; CAA21008.1; -.

BY PIR; T26588; T26588.

WormPep; Y22B12B.6; CE19066.

RO; GO:0005634; C:nucleus; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0003700; F:transcription, DNA-dependent; IEA.

GO; GO:0006350; P:transcription, IEA.

IN RO; GO:0006350; P:transcription, IEA.

RO; GO:0006350; P:transcription; IEA.

RO; GO:0006350; P:transcription; IEA.

RO; GO:0006350; P:transcription; IEA.

RICEPPO; IPR006946; Str ncl receptor.

RICEPPO; IPR001649; Zif_C45teroid.

REPERO; PF00104; Normone rec. 1.

REPERO; PF00104; Normone rec. 1.

REPERO; PF00105; Zif_C45teroid.

REPERO; PF00105; Zif_C45teroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
Nagarajan R., Le N.H., Mahoney H., Araki T., Milbrandt J.D., "Deciphering Peripheral Nerve Myelination Using Schwann Cell Expression Profiling.", Expression Profiling.", the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 31; DB 11; Length 267; 100.0%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gardner A.B.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                       SEQUENCE FROM N.A. STRAIN-CZECH II; TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00047; STROIDFINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 NYGVH 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y32B12B.6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X32B12B.6
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9XX32
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 임
```

```
Query Match
Best Local Similarity 100...
S; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 NYGVH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 NYGVH 109
[1]
SEQUENCE FROM N.A.
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                            FISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8NC30;
Q8NC30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96F19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
Q96F19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8NC30
    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
ProDom; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOL1; 1.
SMART; SM00399; ZnF_C4; 1.
DNA-Dinding; Metal-Dinding; Nuclear protein; Receptor; Transcription; Transcription regulation; Zinc; Zinc-finger.
SEQUENCE 338 AA; 39146 MM; 76526E469D05868A CRC64;
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERGIN-AS (2) M. 145;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=1200953;
MEDLINE-21996410; Meser H.,
Marper D., Risesr H.,
Marphy L., Oliver K., O'Neil S.,
Huang C.-H., Kisesr T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajanderam M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 12, Last annotation update)
Hypothetical protein FLJ14971 (Hypothetical protein FLJ14951).
Homo sapiens (Human).
Homo sapiens (Apparazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TAXID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 31; DB 16; Length 371; 100.0%; Pred. No. 98; 0; Indels (
                                                                                                                                                      100.0%; Score 31; DB 5; Length 338;
100.0%; Pred. No. 88;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 AA; 39201 MW; 5A54095CBFCD8C27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative secreted peptidase.
SCO7521 OR SCBAC25F8.13C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 AA
                                                                                                                                                                                                                                                                                                                                                                                                     371 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro, IPR001466; Beta lactamase. Pfam; PF00144; beta-lactamase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coelicolor A3(2).";
Nature 417:41-147(2002).
EMBL; AL939131; CAC42148.1; -.
HSSP; P15555; ICEF.
                                                                                                                                 Query Match
Best Local Similarity 100...
Lag 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity الاست
نمو 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 NYGVH 230
                                                                                                                                                                                                                                                                         26 NYGVH 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BTV4;
                                                                                                                                                                                                                                                                                                                                                                                                     093129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BTV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
29BTV4
1D 09BTV
AC 09BTV
DT 01-UU
DT 01-UU
DT 01-UC
DE HYPO
OC EUKBY
OC NGBM
                                                                                                                                                                                                                                                                                                                                                        RESULT 9
10931
10031
101-D
101
    8 K K K K K K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Otom T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K., Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

Hypothetical protein.

SEQUENCE 400 AA, 44859 MW, 14F5401ADF9C32A6 CRC64;
                                                                                                                          TISSUB-Thyroid, and Placenta;

TISSUB-Thyroid, and Placenta;

TISSUB-Thyroid, and Alayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Wakamateu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

WNEDO human cDMA sequencing project.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AR027877; BAB55348.1;

EMBL; AK027757; BAB55348.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 31; DB 4; Length 400; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 31; DB 4; Length 400; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
Straugberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 400 AA; 44875 MW; 70FDDD4ED1AA11DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q56F19;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ90529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400 AA
```

```
Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 NYGVH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NYGVH 5
                                                                                                                                                                                                                                                                           Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8PKV6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8PKV6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
108 PKV6
10 08 PKV
AC 08 PKV
DT 01-0C

        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=2108566; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotai, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s.
                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AL136916; CAB66850.1; -.
Hypothetical protein.
SEQUENCE 400 AA, 44831 MW, BD998B0BB73120E4 CRC64;
                                                                                                                                                                                                                                                Query Match
100.0%; Score 31; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 31; DB 4; Length 400; 100.0%; Pred. No. 1.1e+02; Live 0; Mismatches 0; Indels-
                                                                                                TISSUE-Oterus,
Straubberg R.;
Straubberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011719, AAH11719.1; -.
Hypothetical protein.
SEQUENCE 400 AA; 44847 MW; BD89DB4BB7313GF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9DBS1,
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1200015A22Rik protein (RIKEN cDNA 1200015A22 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16,
16,
22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
Hypothetical protein.
DKFZP586G1919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09H076;
01-MAR-2001 (TrEMBLrel.
                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                  105 NYGVH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 NYGVH 109
                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=10090;
                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9H076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9DBS1
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                            940H6D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9DBS1
  SWARRANGO
                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                         쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
STRAIN=306 / ATCC 13902 / XV 101;

STRAIN=306 / ATCC 13902 / XV 101;

MEDLINE=20202145; PubMed=12024217;

A a Silva A.C.R., Ferro J.A., Rethach F.C., Farah C.S., Furlan L.R.,

A a Silva A.C.R., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Alves L.M.C., do Amaral A.M., Bartolnin M.C., Camargo L.E.A.,

A Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA caraid J.B., Ferrelara A.J.S., Ferreira R.C.C., Ferro M.I.T.,

A ratia J.B., Ferrelara A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Rorali B.C., Madiania J., Madeira A.M. B.N., Martinez-Rossi N.M.,

Martins E.C., Madiania J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Roreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

Setubal J.C., Kitajima J.P.,

"Comparison of the genomes of two Xanthomonas pathogens with differing Nature 417459-463 (2002).
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fuents S., Matsuo Y., Nikaido I., Peoslo G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake O., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Ramiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Maring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Maschia M., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Havachia K., Mang K.H., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xanthomonas axonopodis (pv. citri).
Bacteria; Forebacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
VGHI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 31; DB 11; Length 400; 100.0%; Pred. No. 1.1e+02; ative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (MAR.2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO04778; BAB23556.1; -.
EMBL; BC024933.1; -.
MGD; MGI:1921372; 1200015A22Rik.
SEQUENCE 400 AA; 44783 MW; 5A9732B4214D4316 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR006076; Fad_oxred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE011840; AAM36913.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.00
Best Local Similarity 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
```

```
Thu Oct 14 09:36:56 2004
```

```
Query Match
100.0%; Score 31; DB 16; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps.
Pfam; PF01266; DAO; 1.
Complete proteome.
SEQUENCE 403 AA; 44543 MW; A8394D0E38880EEF CRC64;
                                                                                                                                                                                                                               Search completed: October 6, 2004, 16:33:42 Job time: 22.7544 secs
                                                                                                                                       1 NYGVH 5
|||||
163 NYGVH 167
     DR
SQ
                                                                                                                                           S G
```

0;

norv

```
WEDLINE=86108304; PubMed=3943519;

WEDLINE=86108304; PubMed=3943519;

Hoejrup P., Andersen S.O., Roepstorff P.;

Hoejrup P., Andersen S.O., Roepstorff P.;

Totalation, characterization, and N-terminal sequence studies of

Totalation, characterization, and N-terminal

Bur. J. Blochem. 154:153-159(1986).

L. FUNCTION: Component of the cuticale of migratory locust which

contains more than 100 different structural proteins.

L. DOMAIN: The tetrapeptide (A-A-P-[AV]) repeats found throughout the

protective envelope of other species.

Protective envelope of other species.

C. ISIMILARITY: Contains 1 cuticle consensus domain.

PROSTIS: S06038.

PROSTIS: PRO00479; CUTICLE:

REPEAT 22 22

TREPEAT 22 22

TREPEAT 22 22

TREPEAT 22 33

TREPEAT 23 33

TREPEAT 23 33

TREPEAT 23 33

TREPEAT 23 33
                         staphylococ
staphylococ
pleuronecte
                                                                                                                                 xenopus lae
drosophila
                                                                 escherichia
 staphylococ
                                                                                            mus musculu
                                                                             drosophila
                                                                                                                       salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90073593; PubMed=2590176; Klarskov K., Hoejrup P., Andersen S.O., Roepstorff P.; Klarskov K., Hoejrup P., Andersen S.O., Roepstorff P.; Plasma-desorption mass spectrometry as an aid in protein sequence determination. Application of the method on a cuticular protein from the migratory locust (Locusta migratoria)."; Biochem. J. 262:923-930(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                      rattus
                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Cuticle protein 8 (Lin-8) (Lin-ACP 8).
Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroides; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oethoptera; Caelifera; Acridomorpha;
NCBI_TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
           Q9ez11
Q8nws4 s
Q8nws4 s
Q35035 s
Q24533 d
P02340 s
Q010361 r
Q008022 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 1; Length 148;
Pred. No. 5.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C6EADC27C593ACE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ő
                                                                                                                                                                                                                                                         148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                      ALIGNMENTS
DAPB STAAM
DAPB STAAU
DAPB STAAW
DAPB STAEP
TRYP PLEPL
OMPG ECCLI
DICH DROME
PS3 MOUSE
PS3 RAT
                                                                                                                   YJGN SALTY
PPAS XENLA
092A DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ů.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
22
31
31
40
47
15224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Gost Local Similarity 100...
Best Local Si Conservative
                                                                                                                                                                                                                                                         STANDARD;
 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE OF 1-56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NYGVH 68
1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
                                                                                                                                                                                                                                                        CU08 LOCMI
                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE.
 REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                              RESULT 1
 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homo sapien
mus musculu
brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo sapien
b tyrocidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leptospira
bacillus su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chlamydia m
chlamydia t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P11734 locusta mig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homo sapien
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  salmonella
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ricinus com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synechococc
thermoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          schizosacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anabaena sp
                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                        Search time 3.07018 Seconds (without alignments) 84.800 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P449191

P54266

C034206

C0342139

C035139

P513139

P513139

P61771

P61771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P25270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P01821
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                           141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYMZ_HUMAN
TYCC_BREPA
CARA_LEPIN
PUCJ_BACSU
AMYI_SCHPO
KALM_HUWAN
FREI_YEAST
HV3J_HUWAN
FNUM_CABEL
NDF6_HUMAN
NDF6_HUMAN
NDF6_MOUSE
TRKH_SALITY
CAOP_CABEL
AT19_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BRARE
BRARE
BLOOAB
RICCO
RICCO
FHUMAN
CECCLI
                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                  summaries
                                                                                           October 6, 2004, 16:21:13
                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAOP
AT19
AT19
HXC5
ETFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERF
                                                                                                                                                                                                                                                                                                                                      Minimum Match 0%
Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                  Listing first 45
                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
                                                                                                                                             US-09-635-974A-2
31
1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                             SwissProt_42:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing:
                                                                                                                                                                                                                                                                                                seq
sed
                                                                                                                                                                                                   Scoring table:
                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                           Searched:
                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
No.
```

```
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                         YYS3 CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYM2 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYOM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
                                                    RESULT
                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pets6-his3-dedl gene region.";
Nucletc Acids Res. 13:8587-8661(1985).
Nucletc Acids Res. 13:8587-8661(1985).
PUNCTION: Encodes an essential ribose methyltransferase that specifically modifies to 2'-O-methylguanosine a universally conserved nucleotide, G-2270, in the peptidyl transferase center of the mitochondrial large ribosomal RNA (218). This modification seems to be important for the normal accumulation of this latter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGD; S0005727; PET56.
GO; GO:0005739; C:mitochondrion; IDA.
GO; GO:0005889; F:rRNA (guanine-N1-)-methyltransferase activity; IDA.
GO; GO:0000154; P:rRNA modification; IDA.
InterPro; IPR00441; rRNA methylase.
InterPro; IPR001537; SpoU_methylase.
PF00588; SpoU_methylase.
                                                                                                   01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ribose methyltransferase PET56 (EC 2.1.1.) (Mitochondrial large ribosomal RNA ribose methylase) (21S rRNA [GM2251] 2'O-
                                                                                                                                                                                                                                                                                                                                                                                                                        Sirum-Connolly K., Mason T.L.; "Functional requirement of a site-specific ribose methylation in
                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence and transcriptional mapping of the yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 1; Length 412;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodon, PD001244, Spourmethylase; 1.
TIGRRAMs, TIGR00186; rRNA methyl 3; 1.
Mitochondrion; Transferase; Methyltransferase.
SEQUENCE 412 AA; 46387 MW; C01B10254C0EDEA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Scc. 100.0%; Pred. No. 15, ... 0; Mismatches
                            412 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: TO S.POMBE SPECI347.13C.
                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94090319; PubMed=8266080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86093663; PubMed=3001645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L19947; AAA74564.1; --
EMBL; X03245; CAA27002.1; --
EMBL; Z75107; CAA99414.1; --
PIN; S48881; S48881.
GermOnline; 143789; --
SGD; S0005727; PET56.
                                                                         01-MAY-1992 (Rel. 22, Created)
01-FEB-1996 (Rel. 33, Last seq
30-MAY-2000 (Rel. 39, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 262:1886-1889(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [3]
SEQUENCE OF 1-95 FROM N.A.
                               STANDARD;
                                                                                                                                                                                                 methyltransferase).
PETS6 OR YOR201C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932
                          PT56 YEAST
P25270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribosomal
PTS6 | TES |
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Myomesin 2 (M-protein) (165 kDa titin-associated protein) (165 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dolo Digital Marazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Fominidae; Homo.
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAND-Bristol N2;
Du Z., Gatheristol N2;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the ELO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 31; DB 1; Length 435; 100.0%; Pred. No. 16; 0; Indels cive 0; Mismatches 0; Indels
                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-2093 (Rel. 31, Last annotation update)
Hypothetical 51.5 kDa protein D2024.3 in chromosome IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51480 MW; F7940A74A1969914 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUB-Skeletal muscle;
MEDLINE=94095665; PubMed=7505783;
Vinkemeler U., Obermann W., Weber K., Fuerst D.O.;
       435 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1465 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE, PS01188; ELO; 1.
Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WormPep; D2024 3; CE04292.
InterPro; IPR002076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        connectin-associated protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U41011; AAA82288.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; T34200; T34200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 NYGVH 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103
239
278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996
10-OCT-2003
YYS3 CAEEL
P491<u>9</u>1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYM2 HUMAN
PS4296;
```

5; Conservative

Matches

ö

Gaps

; 0

0; Indels

parabrevis

```
-
     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 42, Last amnotation update)
10-OCT-2003 (Rel. 42, Last amnotation update)
17yrocidine syntherase III [Includes: ATP-dependent glutamine adenylase (AsnA) (Glutamine activase); ATP-dependent tyrosine adenylase (TyrA) (Tyrosine activase); ATP-dependent valine adenylase (ValA) (Valine activase); ATP-dependent valine adenylase (Ornithline activase); ATP-dependent crnithine adenylase (Crnithline activase); ATP-dependent leucine adenylase (Leucine TYCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
"The globular head domain of titin extends into the center of the sarcomeric M band. cDNA cloning, epitope mapping and immunoelectron microscopy of two titin-associated proteins.";

J. Cell Sci. 106:319-330(1993).

-!- FUNCTION: Major component of the vertebrate myofibrillar M band. Binds myosin, titin, and light meromyosin. This binding is dose
                                                                                                                                                                                                                                                                                                                                                                                                                                Ide protein, Thick filament, Repeat.
Id-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 5.
                                                                                 -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 5 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 1; Length 1465; Pred. No. 51; 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                        R HSSP; P40189; D30.
R HSSP; P40189; D30.
R Genew; HGNC: 614; MYOM2.
R MIM; 603509; ---.
DR GO; GO: 0008307; F: structural constituent of muscle; TAS.
CO; GO: 000836; F: muscle contraction; TAS.
DR InterPro; IPR003861; FN_III-like.
DR InterPro; IPR003861; FN_III-like.
DR InterPro; IPR003961; FN_III-like.
DR InterPro; IPR003961; FQ-II-like.
DR InterPro; IPR00398; Ig_c2.
DR Ffam; PF00041; fn3; 5.
DR Pfam; PF00041; fn3; 5.
DR Pfam; PF00047; ig; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
W, 6F2927B5AlE69F2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 6486 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MM:
                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG'LIKE; 5.
mmunoglobulin domain; Muscle )
OMAIN 154 245 IO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                 EMBL; X69089; CAA48832.1; -. PIR; S43529; S43529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                  PRINTS, PRODO14; ENTYPE
SMART, SMODGO; EN3; 3.
SMART; SMOG408; IGC2; 1
PROSITE; PS50835; IG_LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 NYGVH 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYCC_BR
030409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 5
BREPA
 ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANGOUS: TYROCIDINE IS A MIXTURE OF FOUR CYCLIC DECAPEPTIDES, TYROCIDINE A (D-PHE-PRO-PHE-D-PHE-ASN-GLN-TYR-VAL-ORN-LEU), B, C, AND D, IN WHICH PHE, AT POSTTIONS 3, 4, AND TYR RESIDUES ARE GRADUALLY REPLACED BY TRP, DEPENDING ON THE RELATIVE CONCENTRATIONS OF THESE AMINO ACIDS IN THE GROWTH MEDIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE
                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 8185 / IAM 1031 / IFO 3331 / NCDO 717 / NCIB 8598;
STRAIN=ATCC 8185 / Dubmed=9352938;
MOCIZ H.D., Marahiel M.A.;
"The tyrocidine biosynthesis operon of Bacillus brevis: complete nucleotide sequence and biochemical characterization of functional
                                                                                                                                                                                                                                                                                      internal adenylation domains.";
J. Bacteriol. 179:6843-6850(1997).
-!- FUNCTION: INCORPORATES SIX AMINO ACIDS (FOR TYROCIDINE A, ASN, GLN, TYR, VAL, ORN, AND LEU) IN THEIR L-CONFIGURATION INTO THE PEPTIDE PRODUCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- PATHWAY: Cyclic peptide antibiotic tyrocidine biosynthesis.
-1- SUBUNIT: LARGE MULTIENZYME COMPLEX OF TYCA, TYCB AND TYCC.
-1- DOMAIN: CONSISTS OF SIX MODULES, AND HARBORS A PUTATIVE
THIORSTERAGE DOWAIN AT ITS C-TERMINAL END. EACH MODULE
INCORPORATES ONE AMINO ACID INTO THE PEPTIDE PRODUCT AND CAN B
FURTHER SUBDIVIDED INTO DOMAINS RESPONSIBLE FOR SUBSTRATE
ADENYLATION THIOLATION, CONDENSATION (NOT FOR THE INITIATION
MODULE), AND EPIMERIZATION (OPTIONAL), AND N METHYLATION
(OPTIONAL).
Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contains 6 covalently bound phosphopantetheines (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN 1 (ASPARAGINE-ACTIVATING).
DOMAIN 2 (GLUTAMINE-ACTIVATING).
DOMAIN 3 (TYROSINE-ACTIVATING).
DOMAIN 4 (VALINE-ACTIVATING).
DOMAIN 5 (ORNITHINE-ACTIVATING).
DOMAIN 6 (LEUCINE-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 3.
ACYL CARRIER (ACP) 3.
ACYL CARRIER (ACP) 4.
ACYL CARRIER (ACP) 4.
ACYL CARRIER (ACP) 5.
ACYL CARRIER (ACP) 5.
ACYL CARRIER (ACP) 5.
ACYL CARRIER (ACP) 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0154; AMPBINDING,
PROSITE; PS00012; PHOSPHOPANTETHEINE; 6.
PROSITE; PS00455; AMP BINDING; 6.
PROSITE; PS50075; ACP DOMAIN; 6.
Ligase; Antibiotic biosynthesis; Phosphopantetheine;
Multifunctional enzyme; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 6 acyl carrier domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; Interpro; InterPro; InterPro; IPR001242; Condensath.
InterPro; IPR001242; Condensath.
InterPro; IPR006163; Pp.bind.
InterPro; IPR006163; Pp.Bind.
InterPro; IPR001031; Ph.Gesterase.
Pfam; PF00650; Pp.Phinding; 6.
Pfam; PF00650; pp.binding; 6.
Pfam; PF00650; pp.binding; 6.
Pfam; PF00550; Thioesterase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF004835; AAC45930.1; -. PDB; 1DNY; 17-MAY-00.
                              NCBI_TaxID=54914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25536
35536
56536
20007
20007
5124
6167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
```

GLUTAMINE AMIDOTRANSFERASE. GATASE (BY SIMILARITY).

```
TIGRFAMS; TIGRO1368; CPSaseIIsmall; 1.
PROSITE; PSO0442; GATABE_TYPE_1; 1.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase;
Glutamine amidotransferase; Complete proteome.
                                                                                 174 363 GLUTAMINE AMIDOTRANSFERASE
253 253 GATASE (BY SIMILARITY).
363 AA, 40261 MW, 58BD2BB8F43D0BEE CRC64;
                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                       61 NYGIH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis
                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1423;
                                                                                                                                                                                                                        1 NYGVH
                                                                                                                                                                                                                                                                                                                                          PUCJ BACSU
032139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria;
                                                                                   DOMAIN
ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION
                                                                    DOMAIN
                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                             PUCJ BACSU
                                                                                                                                                                                                                                                                                                           RESULT 7
   STFFFS
                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the carA family.
-!- SIMILARITY: Concains 1 type-1 glutamine amidotransferase domain.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN=5601 / Serogroup Icterohaemorrhagiae / Serovar lai;

STRAIN=5601 / Serogroup Icterohaemorrhagiae / Serovar lai;

MEDLINE=22598143; PubMed=12712204

Ren S.-X., Fu G., Jiang X.-G., Zang R., Miao Y.-G., Xu H.,

Zhang Y.-X., Gu W.-Y., Zhang Y.-Q., Gai Z., Sheng H.-H., Yin H.-F.,

A zhang Y., Zhu G.-F., Wan M., Hang H.-L., Qian Z., Wang S.-Y., Ma W.,

Xo Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

Xu J.-G., Zhao G.-P.;

"Unique physiological and pathogenic features of Leptospira

Interrogans revealed by whole-genome sequencing.";

Inture 422.888-893(2003).

C. -I. CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +

Dhosphate + glutamate + carbamoyl phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis; first step.
-!- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira
                                                                                                                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain)
PHOSPHOPANTETHEINE (BY SIMILARITY)
                                                                                                                                                                           .
0
                                                                                                                                       Length 6486;
                                                                                                                                                                       0; Indels
                                                                                                      CRC64;
                                                                                                      724011 MW; 4934900AF07DF786
                                                                                                                                       100.0%; Score 31; DB 1; I 100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                               363 AA
                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP, MF_01209; -; 1.
InterPro; PRR06624; CarA_synth_smal
InterPro; IPR066247; CP_synthGATase.
InterPro; IPR001317; CP_synthSmall.
InterPro; IPR000991; GATase_1.
Pfam; PF00988; CPSase_sm_chain; 1.
Pfam; PF00117; GATase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE011305; AAN48438.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00099; CPSGATASE.
PRINTS; PR00096; GATASE.
                                                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                               STANDARD;
                     2037
3075
4110
5154
6197
                                                                                                          Ä.
                                                                                                                                                                                                                                          2664 NYGVH 2668
                                                                                                                                                                                                          1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarīty).
                       2037
3075
4110
5154
6197
6486
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARA OR LA1239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                             RESULT 6
CARA_LEPIN
ID _CARA_LEPIN
                                                                                      BINDING
                     BINDING
BINDING
BINDING
     BINDING
                                                                        BINDING
                                                                                                                                                                                                                                                                                                                                            Q8FGRZ;
                                                                                                                                                                                                                                                                                                                                   SETTETES
                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                          d
```

```
RAY KUNDINE-S9044033; PubMed=9384377;

Runst F., Ogasawara N., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Barselor L., Brans A., Braun M., Brighell S.C., Bron S., Bruschic V., Connerton I.F., Cummings N.J., Daniel R.A., Brhilos S.D., Emmerson P.T., Benisch F.K., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Ray Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Aritz C., Pujita W., Fujita Y., Fuma S., Galizzi A., Galleron N., Fritz C., Pujita W., Fujita Y., Fuma S., Galizzi A., Galleron N., Aritz C., Fujita W., Fujita W., Fuma S., Galizzi A., Galleron N., Aniseppi G., Guy B.J., Haga K., Haleoh J., Harwood C.R., Henaut A., Guiseppi G., Guy B.J., Haga K., Haleoh J., Harwood C.R., Henaut A., Guiseppi G., Guy B.J., Haga K., Haleoh J., Harwood C.R., Henaut A., Goris B., Karamata D., Kasahara Y., Klaert E., Roadsa S., Manen C., Lazarevic V., R. A., Levine A., Liu H., Masuda S., Manen C., Lazarevic V., R. Mediua N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Robot D., O'Reilly M., Portetelle D., Porwollik S., Prescott A.M., Prescott A.M., Prescot R., Rivolta C., Roche B., Roche B., Rosh M., Rayolta S., Schroeter R., Shule B.S., Soldo B., Sekowska A., Sanda E., Roche B., Rosh M., Sadaie Y., Takenchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K., Takenchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K., Munters P., Wipat A., Yamanoto H., Wamine K., Yasamoto H., Wamine K., Yasamoto H., Wamine C., Wasamoto H., Wanier S., Waller E., Wedler E., Weller E., Wedler E., Weller E., Welle
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168;
MEDLINE=21242727; PubMed=11344136;
Schultz A.C., Nygaard P., Saxild H.H.;
"Functional analysis of 14 genes that constitute the purine catabolic pathway in Bacillus subfilis and evidence for a novel regulon controlled by the Puck transcription activator.";
                                                            Gaps
                                                         .
Similarity 80.0%; Pred. No. 22; 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                          Uric acid permease pucJ. PUCJ OR BSU32430.
                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
```

```
CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .

    J. Bacteriol. 183:3293-3302(2001).
    I-PUNCTION: Upptake of uric acid.
    SUBCELLULAR LOCATION: Integral membrane protein (Probable).
    INDUCTION: Expression is very low in excess nitrogen (glutamate plus ammonia) and is induced during limiting-nitrogen conditions (glutamate). Expression is further induced when allantoin or uric acid are added during limiting-nitrogen conditions.
    SIMILARITY: BELONGS TO THE XANTHINE/URACIL PERMEASES FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEE-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OcT-2003 (Rel. 42, Last annotation update)
Probable alpha-amylase C23D3.14c precursor (EC 3.2.1.1) (1,4-alpha-D-SPAC23D3.14C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
MEDLINE=21848401; PubMed=11859360;
MODU V., GWilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros V., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL,
9B97CCC42330C087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 1;
Pred. No. 27;
1; Mismatches C
                                                                                                                                                                                                                                                              Complete proteome.
POTENTIAL.
                                                                                                                                                                                                                                           Pfam, PF00860, xan_ur_permease, 1.
TIGRPAMS, TIGROO801, nce2, 1.
SS01116, SS01116, DERMASE,
Transmembrane, Transport, Complete prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.8%; Score 30;
80.0%; Pred. No. 2
                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                          Subtilist, BG13984; pucJ.
InterPro, IPR06642; Xan ur permease.
InterPro, IPR06643; Xant/urac/vitC.
                                                                                                                                                                                                                                                                                                                                                                                                                                 47100 MW;
                                                                                                                                                                                       EMBL; Z99120; CAB15233.1; ". PIR; E70016; E70016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                      401
449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 NYGIH 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NYGVH 5
                                                                                                                                                                                                                                                                          Transmembrane; T
TRANSMEM 11
TRANSMEM 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMY1 SCHPO
Q09840;
                                                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                           FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMY1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
 ਨੇ
```

```
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,
RA Goliver K., C'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders B., Seger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Gabel C., Fuchs M., Fritzc C., Helzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Helzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Helzer E., Moestl D., Hilbert H.,
RA Gorzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Hels Rey F., Benito J.,
RA Crutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
R. The genome sequence of Schizosaccharomyces pombe.",
R. Maure 41:S191-880(2002).
RA Maure 41:S191-880(2002).
RA C. - CARANTIC ACTIVITY: Endohydrolysis of 1,4-lpha-glucosidic
Linkages in oligosaccharides and polysaccharides.
C. - CARANTIC ROTHIAIS C. C.
Hinkages in oligosaccharides and polysaccharides.
C. - CIRANTY: Belongs to family 13 of glycosyl hydrolases.
C. - SIMILARITY: Belongs to semilarity 1 and the content and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z64354; CAA91249.1; -...
PIR; T38299; S62505.
HSSP; P10259; TAAA.
GeneDB SPOWDe; SPAC23D3.14c; -.
InterPro; IPR006589; Alp amyl cat sub.
InterPro; IPR00647; Alpha amylact.
Ffam; PR00128; alpha-amylase; i...
SMART; SM00642; Aamy; Laxbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE ALPHA-AMYLASE C23D3.14C.
BY SIMILARITY.
BY SIMILARITY.
CALCIUM 1 (BY SIMILARITY).
CALCIUM 2 (BY SIMILARITY).
CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
CALCIUM 2 (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FE9DE99D323E1890 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB 1
Pred. No. 35;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 BY
191 BY
311 BY
291 N-:
332 N-
67004 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435 NYGIH 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NYGVH 5
```

φ

us-09-635-974a-2.rsp

```
X-linked Kallmann's syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
373
540
680 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              514
                                                               activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
  MEDLINE=92005720, PubMed=1913827,
Legouis R., Hardelin J.-P., Levilliers J., Claverie J.-M., Compain S.,
Wunderle V., Millasseau P., le Pasalier D., Cohen D., Caterina D.,
Bougueleret L., Delemarre-Van de Waal H., Lutfalla G., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure of the X-linked Kallmann syndrome gene and its homologous pseudogene on the Y chromosome."; Nat. Genet. 2:305-310(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-71 FROM N.A.
MEDLINE=96069588; PubMed=7590336;
Cohen-Salmon M., Tronche F., del Castillo I., Petit C.;
"Characterization of the promoter of the human KAL gene, responsible for the X-chromosome-linked Kallmann syndrome.";
Gene 164:235-242(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Initial characterization of anosmin-1, a putative extracellular matrix protein synthesized by definite neuronal cell populations in the central nervous system."; the central nervous 179:1787(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hardelin J.-P., Levilliers J., Blanchard S., Carel J.-C.,
Leutenegger M., Pinard-Bertelletto J.-P., Bouloux P., Petit C.,
"Heterogeneity in the mutations responsible for X chromosome-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [3] SEQUENCE FROM N.A. MSGUENCE FROM N.A. MEDLINE=92018217; PubMed=1922361; Franco B., Guioli S., Pragliola A., Inceri B., Bardoni B., Franco B., Guioli S., Maetrini E., Pieretti M., Taillon-Miller P., Brown C.J., Willard H.F., Lawrence C., Persico N.G., Camerino G., Ballabio A.; Agena deleted in Kallmann's syndrome shares homology with neural cell adhesion and axonal path-finding molecules."; Mature 353:529-536(1991).
                                                                                                     01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Anosmin 1 precursor (Kallmann syndrome protein) (Adhesion molecule-
                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                            "The candidate gene for the X-linked Kallmann syndrome encodes a protein related to adhesion molecules."; cell 67:423-435(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96429296; PubMed=8832397;
Soussi-Yanicostas N., Hardelin J.-P., del Mar Arroyo-Jimenez M.,
Ardouin O., Legouis R., Levilliers J., Traincard F., Betton J.-M.
Cabanie L., Petit C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VALIANT KALI LYS-514, AND VARIANT VAL-534.
MEDINNE-98251583; PubMed-9589672;
MAya-Nunez G., Zenteno J.C., Ulloa-Aguirre A., Kofman-Alfaro S.,
Mendez J.E.;
"A recurrent missense mutation in the KAL gene in patients with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
MEDLISIONS.
MEDLINE-93265164; PubMed=1303284;
del Castillo I., Cohen-Salmon M., Blanchard S., Lutfalla G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [6]
VARIANT KALI LYS-267, AND VARIANT VAL-534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93278384; PubMed=8504298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hum. Mol. Genet. 2:373-377(1993).
                                                                                 01-NOV-1991 (Rel. 20, Created)
01-DEC-1992 (Rel. 24, Last seq
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                     like x-linked).
KALI OR KAL OR ADMLX OR KALIGI
                                            STANDARD;
                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kallmann syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                       KALM HUMAN P23352;
                                            HERE THE SET THE SET OF THE SET O
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:-SUBCELLULAR LOCATION: Secreted. Localized at cell surface.
-:- PTM: N-glycosylated.
-:- DTM: N-glycosylated.
-:- DISEASE: Defects in KALl is the cause of Kallmann syndrome 1
-- DISEASE: Defects in SALl is the cause of Kallmann syndrome 1
-- KALL) [MIM: 308700], also abbreviated KS. KALL is a genetic
disorder that associates hypogonadotropic hypogonadism and
anosmia. In this disease, the normal embryonic migration of GNRH-
synthesizing neurons from the olfactory placodes to the
hypothalamic region as well as the axonal extension of olfactory
neurons cowards the forebrain are impaired.
-- SIMILARITY: Contains 1 WAP-type domain.
J. Clin. Endocrinol. Metab. 83:1650-1653(1998).
-!- FUNCTION: May be an adhesion-like molecule with anti-protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00317; 4 DISULFIDE CORE; 1.
Cell adhesion; Glycoprotein; Serine protease inhibitor; Repeat; Signal; Polymorphism; Disease mutation.
SIGNAL 1 20 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> K (IN REF. 3).
-> R (IN REF. 3).
5D6ACC9F14B5F5F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIRRONBCTIN TYPE-III 1.
FIBRONBCTIN TYPE-III 2.
FIBRONBCTIN TYPE-III 3.
FIBRONBCTIN TYPE-III 4.
N-LINED (GLCNAC...) (P.
N-LINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N -> K (in KALI).
/FTIG=VAR 007720.
E -> K (in KALI).
/FTIG=VAR_012742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR 007721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANOSMIN 1.
"CYSTEINE BOX".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NN -> VR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    540 A
76066 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534
```

```
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 70 Nubmed=9169871;

MEDLINE=97313267; PubMed=9169871;

MEDLINE=97313267; PubMed=9169871;

A Dohnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Brian K.-D., Floeth M., Goffeau A., Heblaing U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Meller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., A. Porteelle D., Purnelle B., Rechmann E., Schwarz S., Scharz S., Scharz S., Scharz S., Unrestarazu L.A., Vandenbol M., Verhasselt P., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; Weller H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; Then nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=F113;
MEDLINE=92237270; PubMed=1570306;
Dancis A., Roman D.G., Anderson G.J., Hinnebusch A.G., Klausner R.D.;
Ferric reductase of Saccharomyces cerevisiae: molecular
characterization, role in iron uptake, and transcriptional control by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Inorg. Biochem. 47:249-255(1992).
-!- FUNCTION: Reductase activity that acts on ferric iron chelates external to the cell. Plays a role in iron uptake. May participate in the transport of electrons from cytoplasm to an extracellular substrate (ferric ion) via FAD and heme intermediates. May also participate in Cu(II) reduction and Cu(I)
                                                Gaps
                                                                                                                                                                                                                       01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ferric reductase transmembrane component 1 precursor (EC 1.16.1.7)
(Ferric-chelate reductase 1).
FREI OR YLR214W OR L8167.2.
                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Ferric iron reduction and iron assimilation in Saccharomyces cerevisiae.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: NADH + 2 Fe(3+) = NAD(+) + 2 Fe(2+).
-!- COFACTOR: FAD (Probable).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- INDUCTION: BY IRON DEPRIVATION. REPRESSED BY IRON UPTAKE.
-!- SIMILARITY: Belongs to the FRE / CYBB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
MEDLINE=99057491; PubMed=1431884;
Anderson G.J., Lesuisse E., Dancis A., Roman D.G., Labbe P.,
Klausner R.D.;
             DB 1; Length 680; 41;
                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 89:3869-3873(1992).
                                                                                                                                                                                           686 AA.
                                            Mismatches
             Score 30;
Pred. No.
            96.8%;
                                            Conservative
                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 387:87-90(1997).
            Query Match
Best Local Similarity
                                                                                             |||:|
224 NYGIH 228
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                           1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                           YEAST
                                                                                                                                                           RESULT 10
FRE1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iron."
                                         Matches
                                                                                                                                                                                           ò
                                                                                                         임
```

```
..
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FERRIC REDUCTASE TRANSMEMBRANE COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                               GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:000293; F:ferric-chelate reductase activity; IDA.
GO; GO:0012677; P:copper ion import; IDA.
GO; GO:0006826; P:iron ion transport; IDA.
InterPro; IPR002916; Ferric reduct.
InterPro; IPR0194; Ferric reduct.
Oxidoreductase; Electron transport; Transmembrane; Iron transport; STGNAL
SIGNAL
FAD; NAD; Copper; G1voprotein; Signal; Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 18:553-560(1979).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 1; Length 686; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7F6BB3B93A95D6A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
"Amino acid sequence of the VH region of human myeloma
cryoimmunoglobulin IgG Hil.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02054; G1HUHL.
HSSP, P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
N-LINKED (GLCNAC.).
N-LINKED (GLCNAC.).
N-LINKED (GLCNAC.).
N-LINKED (GLCNAC.).
N-LINKED (GLCNAC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAD (POTENTIAL).
NAD (POTENTIAL).
1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; PO1772; ZFB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=79124695; PubMed=420800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78853 MW;
                                                                                                                                            EMBL; M86908; AAA34608.1; -. EMBL; U14913; AAB67424.1; -. PIK; S30075; S30075. Germonline; 142276; -. SGD; S0004204; FREI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 NYGIH 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HV3J_HUMAN
P01771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
NP_BIND
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HV3J HUMAN

ID HV3J HUMAN

ID DT 21-UUL

DT 10-OCT

DE IG HORD SE

OC ENEARY

OC MAMMAIL

ON (11)

RP SEQUENT

RA Chiu Y

RT "Amino

RT "Amino
```

23 KDA

ö

Gaps

ö

RURE RESERVED SON

ò g

```
Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
A pukuzumi Y., Fujimori Y., Komiyama M., Ishis S., Yamamoto J.,
A tanashita H., Marsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
A wagatauma M., Murakawa K., Kanahori K., Takahashi-Fujii A., Oshima A.,
Bugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
Masuho Y., Nagai K., Isogai T.,
Masuho Y., Nagai K., Isogai T.,
Whith B., Suzuki Y., Sugano S., Nagahari K.,
Masuho Y., Nagai K., Isogai T.,
Whith E., Nagai K., Isogai T.,
Whith E., Nagai K., Isogai T.,
Whith E., Masuho Y., Nagai K., Isogai T.,
Whith E., Masuho Y., Nagai K., Isogai T.,
Whith E., May be a trans-acting factor involved in the development
and maintenance of the mammalian nervous system. Transactivates
the promoter of its own gene (By similarity).
C. I. SUBUNIT: Efficient DNA binding requires dimerization with another
DHIH Protein (By similarity).
C. I. SUBUNIT: Lacquence differs (Probable).
C. I. SUMILARITY: Contains I basic helix-loop-helix (bhiH) domain.
C. I. CAUTION: Ref. I sequence differs from that shown due to frameshifts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                  113 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
116 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
127 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
128 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
159 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
158 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
158 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
158 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
150 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
150 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
150 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
PROSITE; PS00198; 4FE4S FERREDOXIN; 2.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide;
Iron-sulfur; 4Fe-4S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-WAR-2004 (Rel. 43, Last annotation update)
Neurogenic differentiation factor 6 (NeuroD6) (My051 protein)
                                                                                       MITOCHONDRION (BY SIMILARITY).
NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 1; Length 212;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mao Y.M., Xie Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 37;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6-HUMAN STANCE.
NDF6 HUMAN STANCE.
296NK81, 09H3H6;
28-FEB-2003 (Rel. 41, Last seque
f 28-FEB-2003 (Rel. 41, Last seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in positions 300 and 307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                           212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                     212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 NYGLH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                            rissum=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                 TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEURODE
                                                                                                                                                                                                                                                                                METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                        METAL
                                                                                                                                 CHAIN
                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
            STATESTATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           င်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A PART A 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hough R.F., Lingam A.T., Bass B.L.; "Caenorhabditis elegans mRNAs that encode a protein similar to ADARS derive from an operon containing six genes."; Nuclaic Acids Res. 27:344-3432(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -I - FUNCTION: May donate electrons to ubiquinone.
-I - CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-I - CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
-I - COFACTOR: Binds 2 4Fe-4S clusters per subunit (By similarity).
-I - SUBUNIT: Complex I is composed of 45 different subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SIMILARITY: Belongs to the complex I 23 kDa subunit family.
-!- SIMILARITY: The iron-sulfur centers are similar to those of
                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                              Length 121;
                                                                                                                                                                                                                                                      PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                    121 AA; 13566 MW; 480FC53610EF5DAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
MADH-ubiquinone oxidoreductase 23 Kba subunit, mitochn (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-23KD) (CI-23KD)
      GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv.; IG.
IRR, ISS 50815; IG Like; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                              Score 28; DB 1;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P00198; 2FDN.
Wormbep; 720445; CE00832.
InterPro; IPR001450; 4Fe4S_ferredoxin.
Pfam; PP00037; fer4; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterial-type 4Fe-4S ferredoxins.
                                                                                                                                                                                                                            IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
MEDLINE=99377169; PubMed=10446229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF140272; AAD34863.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U00037; AAA50662.1;
PIR; T16914; T16914.
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NYGMH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAEEL
                                                                                                                                                                                                                                                   MOD_RES
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T20H4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   022619;
                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUIN
```

```
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                         TRKH ECOLI
                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
  d
                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C57BH/6; TISSUB=Brain;
AMEDLINE-95200803; PubMed=7545978;
ABATHN-C57BH/6; TISSUB=Brain;
AMEDLINE-95200803; PubMed=7545978;
ABATHN-C57BH/6; TISSUB-Brain-specific helix-loop-helix protein with
TWEX-1: a novel brain-specific helix-loop-helix protein with
T "MEX-1: a novel brain-specific helix-loop-helix protein neurons.";
T autoregulation and sustained expression in mature cortical neurons.";
THE TISTUBLIATOR Activates E box-dependent transcription in collaboration
T the promoter of the mammalian nervous system. Transactivates
T SUBUNIT: Efficient DNA binding requires dimerization with another
T SUBCLIGUAR LOCATION: Nuclear (Probable).
T SUBCLIGUAR LOCATION: Nuclear (Probable).
T TISSUE SPECIFICITY: Specific to the nervous system of both embryos and adults. Highest levels in the cortical plate of the cerebrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Neurogenic differentiation factor 6 (NeuroD6) (Atonal protein homolog
2) (Helix-loop-helix protein mATH-2) (MATH2) (NEX-1 protein).
NEUROD6 OR ATOH2 OR ATH2 OR NEXI.
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=129/J;
MEDLIRE=955673; PubMed=7744035;
Shimizu C., Akazawa C., Nakanishi S., Kageyama R.;
"MATH-2, a mammalian helix-loop-helix factor structurally related to
the product of Drosophila proneural gene atonal, is specifically
Expressed in the nervous system ";
Eur. J. Blochem. 229:239-248(1995).
                                                                                                                         Transcription regulation; Activator; DNA-binding; Nuclear protein.

DOMAIN 54 63 POLY-GLU.

DOMAIN 80 86 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                     Score 28; DB 1; Length 337;
Pred. No. 58;
1; Mismatches 0; Indels
                                                                                                                                                               BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF.
6B0F4127AC0F809E CRC64;
or send an email to license@isb-sib.ch)
                          EMBL; AF063609; AAG43167.1; ALT_FRAME.
EMBL; AK055238; BAB70885.1; -.
                                       EMBL, AKOS5238; BAB70885.1; -.. Genew; HGNC:13804; NEDROD6.
InterPror, IPRO01092; HLH basic.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
PROSITE; PS50888; HLH; 1.
                                                                                                                                                                                           38705 MW;
                                                                                                                                                                                                                       90.3%;
                                                                                                                                                                                                      Query Match
Query Match
Best Local Similarity 80.vv.,
Best Local Similarity 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                           337 AA;
                                                                                                                                                                                                                                                                                                       286 NYGMH 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                RESULT 14
NDF6 MOUSE
ID NDF6_MOUSE
                                                                                                                                                                DNA BIND
                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                         P48986;
pp
                                                                                                                                                                                                                                                                              8
```

```
Gaps
                                                                                                                                                                                                                                               Transcription regulation; Activator; DNA-binding; Nuclear protein.

DOMAIN 80 86 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

DNA-BIND 95 106 BASIC DOMAIN.

DOMAIN 107 147 HELIX-LOOP-HELIX MOTIF.

SEQUENCE 337 AA; 38644 MW; 35C18ACD8EE1EFBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=E.coli; STRAIN=K12;
MEDLINE=92358234; PubMed=1379743;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region
Erom 84.5 to 86.5 minutes";
Science 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlosser A., Meldorf M., Stumpe S., Bakker B.P., Epstein W.; "TrkH and its homolog, TrkG, determine the specificity and kinetics of cation transport by the Trk system of Escherichia coli."; J. Bacteriol. 177:1908-1910(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISION TO 69.

SPECIESE.col; STRAIN=K12 / MG1655;

MEDIARE=97426617; bubMd=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P21166; P76769; C1-miles (Created) (1-MX-1991 (Rel. 18, Created) (1-MX-1995 (Rel. 32, Last sequence update) (1-0CT-2003 (Rel. 42, Last annotation update) Trk system potassium uptake protein trkH. TRKH OR B3849 OR Z5371 OR ECS4777 OR SF3925 OR S3827.
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
58;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 1
Pred. No. 58;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=E.coli; STRAIN=K12;
MEDLINE=91057145; PubMed=2243799;
Nakahigashi K., Inokuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95204366; PubMed=7896723;
EMBL; D44480; BAA07923.1; --
EMBL; U29086; AAC14576.1; --
PIR; 1548682; 1458682.
PIR; 157038; 157038.
MGD; MGI:106593; Neurod6.
InterPro; IPR001092; HLH_basic.
Fam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli, Escherichia coli 0157:H7, and
                                                                                                                                                                                                                                                                                                                                                                                                                                           90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 NYGMH 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NYGVH 5
```

```
Respectively could between the fadig gene and the rrmh operon from the schemical could be sequence between the fadig gene and the rrmh operon from the schemical could be seen. In the schemic could be seen. In the sch
```

```
Gaps
                                                                                                                                                                                                .,
     DB 1; Length 483;
                                                                                                                                                                                                Indels
                                                                                                                                                            -> S (IN REF. 4).
1AA9CC2F83EB509A CRC64;
                                                                                                                                            MISSING (IN REF. 2).
V -> IV (IN REF. 4).
C -> S (IN REF. 4).
                                                                                                                                                                                  Score 28; DB 1
Pred. No. 82;
1; Mismatches
                                                                                                                                                                                                                                                  Search completed: October 6, 2004, 16:30:22
                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                      POTENTIAL. POTENTIAL.
                                                                                    POTENTIAL. POTENTIAL.
                                                                                                                               POTENTIAL. POTENTIAL.
                                                                                                                                                                    52959 MW;
                                                                                                                                                                                  90.3%;
80.0%;
                                                                                                                                                                                                 4; Conservative
B65190; B65190
                                                       Complete proteome.
TRANSMEM 9
TRANSMEM 35
TRANSMEM 70
                                                                                                                                                                    483 AA;
                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                             252 NYGLH 256
                                                                                                                                                                                                                                                          Job time : 6.07018 secs
                                                                                                                                                                                                               1 NYGVH 5
                                                                                   TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                         TRANSMEM
TRANSMEM
                                                                                                                                                             SEQUENCE
                                                                                                                                               CONFLICT
                                                                                                                                                                                    Query Match
                                                                                                          FRANSMEM
                                                                                                                  FRANSMEM
                                                                                                                                        FRANSMEM
ઠે
```

·,

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

using sw model - protein search, OM protein October 6, 2004, 16:23:59 ; Search time 5.26316 Seconds (without alignments) 91.382 Million cell updates/sec Run on:

US-09-635-974A-2 31 1 NYGVH 5

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					٠																										
	Description	TOTOTT TOTT	Ig heavy chain V r	Ig heavy chain pre	ticle protein	hypothetical prote	hypothetical prote	protein F56A6.1 [i	hetical	rRNA (guanosine-2'	hypothetical prote	hypothetical prote	probable histidine	-4	165K protein, skel	tyrocidine synthet		C)	ത	hypothetical prote	oute	probable alpha-amy		allmann	ferric reductase (probable membrane	heavy	Ig heavy chain pre	cal pr	tical	hypothetical prote
	9		PH1026	432456	805638	AF2424	F33082	387721	126588	54881	F34200	376734	396500	115179	343529	131076	900266	4B2402	370016	364655	171942	362505	140351	317982	330075	AF0122	GIHUHL	4	2825	1691	9513
	DB																												-		
	Length I		109	139	148	263	325	325	338	412	435	475	482	697	1465	6486	118	170	449	479	479	581	619	680	989	788	121	140	196	212	320
	Ouery		8	8	100.0	8	8	8	8	00	8	8	8	8	8	00	ø	ω	S	8.96	S	S	S	S	la	lo	0	\circ	\circ	\circ	0
	Score	1 1 1 1 1 1	31	31	31	31	31	31	31	31	31	31	31	31	33	31	30	30	30	30	30	30	30	30	30	30	28	28	28	28	28
;	kesuit No.		 4	7	m	4,	Ŋ	9	7	00	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

NEX.1 - mouse gene Dlx-3 protein hymothatical nucte	~	hypothetical prote hypothetical prote	hypothetical prote lactose transport	potassium uptake p probable outer mem	hypothetical prote potassium uptake p	potassium uptake p trk system potassi	hypothetical prote
148682 157038	G91064 D83983	E82401 H75009	G71142 F83990	B65190 B71963	A64546 A91226	G86072 AE0914	AI0684
0100	100	0 0	п г	0 0	0 0	0 0	0
337	352	372	388 425	432 438	450 483	483 483	589
000	90.00 90.30	90.9 80.9	90.3 90.3	90.3	90.3 90.3	90.3 90.3	90.3
00 00 00 00 00 00	3 33 C	7 7 8 8 8	78 78 78	78 78 78	78 78 78	78 78	78
3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	33 34	9 P	337	€. 4. 9. O	4 4 1 2	43 44	45

ALIGNMENTS

-	
ESULT	9H1026

RESULT 1
PH1026
Ig heavy chain V region (clone 163-c3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
R;Tillman, D.M.; Jou.
N. T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Tilles Boch 1903 and 1963 anti-DNA antibodies are the products of clonally selective B A;Accession: PH1026
A;Accession: ph10

Gaps . 0 Query Match 100.0%; Score 31; DB 2; Length 109; Best Local Similarity 100.0%; Pred. No. 8.6; Matches 5; Conservative 0; Mismatches 0; Indels

ö

31 NYGVH 35 1 NYGVH 5 δ DD

A32456

A32456

A32456

G beavy chain precursor V region - mouse

C species: Mus musculus (house mouse)

C species: Mus musculus (house mouse)

C species: Mus musculus (house mouse)

C species: Musculus (house mouse)

C species: A32456

R pombrink-Kurtranan, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.

J. Biol. Chem. 264, 4513.4522, 1989

A;Title: Variable region primary structures of a high affinity anti-fluorescein immunogla A,Reference number: A32456; MUID:89174706; PMID:2494173

A;Refatus: preliminary

A;Residues: preliminary

A;Residues: 1-139 < DOM>

A;Cross-references: GB:J04609; NID:9556316; PIDN:AAA50298.1; PID:9556317

A;Cross-references: GB:J04609; NID:9556316; PIDN:AAA50298.1; PID:9556317

A;Cross-references: GB:J04001 in V region; immunoglobulin homology

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-116/Domain: immunoglobulin homology <INM>

Gaps ö Query Match 100.0%; Score 31; DB 2; Length 139; Best Local Similarity 100.0%; Pred. No. 11; Matches 5; Conservative 0; Mismatches 0; Indels Indels

ò d

```
protein F56A6.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: B87721
R;Accession: B87721
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode A;Title: Genome sequence of the nematode A;Title: A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:chr_I; PIDN:AAC17014.1; PID:g3150502; GSPDB:GN00019; CESP:F56A6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Applications proceed the procession of the proce
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-325 - MUR>
A;Cross-references: EMBL:AF067217; PIDN:AAC17014.1; GSPDB:GN00019; CESP:F56A6.1
A;Experimental source: strain Bristol N2; clone F56A6
             Cispecies: Caenorhabditis elegans
Cipate: 29-oct-1999 #sequence_revision 29-oct-1999 #text_change 29-oct-1999
Riburray, J.; Rohlfing, T.; O'Neal, D.; Wilson, R.
Aibescription: The sequence of C. elegans cosmid F56A6.
Aibescription: T33082
Aibescription: T33082
Aibescription: T33082
Aibescription: T33082
Aibescription: Dana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 325;
protein F56A6.1 - Caenorhabditis elegans (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 31; DB
100.0%; Pred. No. 26;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 31; DB Best Local Similarity 100.0%; Pred. No. 26; Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 1
A; Introns: 51/1; 135/3; 202/2; 222/2; 262/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Y32B12B.6 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 NYGVH 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 NYGVH 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-325 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: B87721
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: CESP:F56A6.1
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Residues: 1-325 <£
A,Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Note: partial CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Genetics:
A,Gene: F56A6.1
A,Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF2424
AF2424
AF2424
AF2424
AF2424
AF2424
Decrees Nostoc sp. PCC 7120
C.Species: Nostoc sp. PCC 7120
C.Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. Strain PCC 7120
C.Accession: AF2424
C.Accession: AF2424
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriguchi NAkazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A,Reference number: AB1807; MUID:21595285; PMID:11759840
A,Accession: AF2424
A,Accession: AF2424
A,Accession: DNA
                                                                                                                                                                                                                                                                                                   cuticle protein 8 - migratory locust
Cispecies: Locusta migratoria (migratory locust)
Cjate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
Cjacession: 805638; B24802
R/Rlarskov, K.; Hojrup, P.; Andersen, S.O.; Roepstorff, P.
Biochem. J. 262, 923-930, 1989
Ajfitle: Plasma-desorption mass spectrometry as an aid in protein sequence determination
A;Reference number: 805638; MUID:90073593; PMID:2590176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Residues: 1-263 <KUR>
A,Residues: 1-263 <KUR>
A,Cross-references: GB:BA000019; PIDN:BAB76649.1; PID:g17134088; GSPDB:GN00179
A,Experimental source: strain PCC 7120
C,Genetics:
A,Gene: a114950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 31; DB 2; Length 263; 100.0%; Pred. No. 21; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 1-148 < KLA>
R; Hojrup, P.; Andersen, S.O.; Roepstorff, P.
Eur. J. Biochem. 154, 153-159, 1986
A; Reference number: A91157; MJD:86108304; PMID:3943519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 31; DB 1;
100.0%; Pred. No. 12;
cive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Residues: 1-53, "X', 55-56 < HOJ>
C, Superfamily: migratory locust cuticle protein (C, Superfamily: migratory locust cuticle protein (C, Reywords: structural protein (F, 16-19/Region: 4-residue repeat (A-A-P-[AV])
F, 22-25/Region: 4-residue repeat (A-A-P-[AV])
F, 25-31/Region: 4-residue repeat (A-A-P-[AV])
F, 34-47/Region: 4-residue repeat (A-A-P-[AV])
F, 34-47/Region: 4-residue repeat (A-A-P-[AV])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 NYGVH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 NYGVH 68
             ß
                                                                                           50 NYGVH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NYGVH
             NYGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S05638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: B24802
```

g

0

ö

RESULT 5 T33082

Gaps

. 0

```
Cispedies: Synechocystis sp.

Ajvariety: PCC 6803

Ajvariety: PCC 6803

Cipate: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

Rikaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N., O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: S76734
A;Status: preliminary
A;Holcule type: DNA
A;Cross-references: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA18646.1; PID:g165373
A;Cross-references: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA18646.1; PID:g165373
A;Cross-references: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA18646.1; PID:g165373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable histidine decarboxylase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O'Z-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: B96500
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hugher, J.L.; Vi, Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Recius: preliminary
A;Molecule type: DNA
A;Residues: 1-482 cSTO>
A;Residues: 1-482 cSTO>
A;Residues: 1-482 cSTO>
A;Residues: Lagerances: GB:AE005173; NID:97523682; PIDN:AAF63121.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 31; DB 2; Length 475; Best Local Similarity 100.0%; Pred. No. 39; Matches 5; Conservative 0; Mismatches 0; Indels
     submitted to the EMBL Data Library, November 1995
A; Description: The sequence of C. elegans cosmid D2024.
A; Reference number: 221488
A; Accession: T34200
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-435 a 6002>
A; Cross-references: EMBL:U41011; PIDN:AAA82288.1; CESP:D2024.3
A; Genetics: A; 57/3; 306/1; 398/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein - Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S74322; MUID: 97061201; PMID: 8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 31; DB 100.0%; Pred. No. 36; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 NYGVH 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 NYGVH 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rRNA (guanosine-2'-O-)-methyltransferase (EC 2.1.1.-) - yeast (Saccharomyces cerevisiae)
N'Alternate names: mirochondrial large ribosomal RNA methylase; protein 04827; protein Y
C'Species: Saccharomyces cerevisiae
C'Species: Saccharomyces cerevisiae
C'Date: 29-Nov-1994 #seguence revision 12-May-1995 #text_change 21-Jul-2000
C'Accession: 848881; S07682; $67093
Science 262, 1886-1889, 1937
A; Situm-Connolly, K.; Mason, T.L.
Science 262, 1886-1889, 1987
A; Title: Functional requirement of a site-specific ribose methylation in ribosomal RNA.
A; Reference number: 848881; MUID:9409319; PMID:8266080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Genome: nuclear
C;Function:
A;Description: methyltransferase; required for formation of functional mitochondrial rib
C;Keywords: methyltransferase; mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: DNA
A, Residues: 1-95 &STR>
A, Residues: 1-95 &STR>
A, Residues: 1-95 &STR>
A, Cross-references: EMBL:X03245; NID:g3778; PIDN:CAA27002.1; PID:g3779
B, Hughes, B.; Pohl, T.M.
Submitted to the Protein Sequence Database, July 1996
A, Reference number: S6685
A, Residues: 1-412 < Hug.
A, Residues: 1-412 < Hug.
A, Residues: 1-412 < Hug.
A, Cross-references: EMBL:Z75107; NID:g1420472; PID:e252073; FID:g1420475; MIPS:YOR201C
C, Generics:
A, Gener
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: $48881
A,Status: nucleic acid sequence not shown; translation not shown
A,Status: nucleic acid sequence not shown; translation not shown
A,Residues: 1-412 ASIR>
A,References: EMBL:L19947; NID:9431759; PIDN:AAA74564.1; PID:9431760
A;Cross-references: EMBL:L19947; NID:9431759; PIDN:AAA74564.1; PID:9431760
A;Nocle: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
R;Struhl, K.
Nucleic Acids Res: 13, 8587-8601, 1985
A;Title: Nucleotide sequence and transcriptional mapping of the yeast pet56-his3-ded1
A;Reference number: S07681; MUID:86093663; PMID:3001645
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T34200
hypothetical protein D2024.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34200
R;Du, Z.; Gattung, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                         Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 31; DB 2; Length 412; Best Local Similarity 100.0%; Pred. No. 34; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 31; DB 2; Best Local Similarity 100.0%; Pred. No. 28; Matches 5; Conservative 0; Mismatches 0
A, Experimental source: clone Y32B12B
C,Genetics:
A,Gene: CESP:Y32B12B.6
A,Map position: 5
A,Introns: 28/3; 61/1; 257/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 NYGVH 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

·;

```
tyrocidine synthetase 3 - Brevibacillus brevis
Cispecies: Brevibacillus brevis
Cispecies: Brevibacillus brevis
Cispecies: Brevibacillus brevis
Cispecies: Brevibacillus brevis
Cipate: 02-8ep-2000 #sequence_revision 02-8ep-2000 #text_change 01-Dec-2000
Cidacesion: 731076
Miranhiel M.A.
J. Bacteriol 179, 6843-6850, 1997
A;Title: The tyrocidine biosynthesis operon of Bacillus brevis: Complete nucleotide seque A;Reference number: 220969; MUID: 98012987; PMID: 9352938
A;Reference number: 220969; MUID: 98012987; PMID: 9352938
A;Reference number: DAA
A;Residues: DAA
A;Residues: DAA
A;Cross-references: EMBL:AF004835; NID: 92623770; PID: 92623773; PIDN: AAC45930.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-118 <LCD+>
A;Cross-references: GB:M59984
C;Comment: This protein recognizes a restricted idiotype associated with antibodies specific C;Comment: This protein recognizes a restricted idiotype associated with antibodies specific Superfamily: immunoglobulin V region; immunoglobulin Nomology
C;Reywords: heterotetramer; immunoglobulin homology < IMM>
F;15-97/Domain: immunoglobulin homology < IMM>
F;31-35/Region: complementarity-determining 1
F;50-65/Region: complementarity-determining 3
F;98-108/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F.6165-6233/Domain: acyl carrier protein homology <ACP6>
F.1000,2037,3075,4110,5154,6197/Binding site: phosphopantetheine (Ser) (covalent) #statut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ighaavy chain V region (MCI) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-May-1997
C;Accession: PQ0266
R;Lohman, K.L.; Carrillo, M.A.; Kennedy, R.C.
A;Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal A;Reference number: PQ0265; MUID:92039046; PMID:1937027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Pathway: tyrocidine biosynthesis
A, Pathway: tyrocidine biosynthesis
C, Superfamily: acyl carrier protein homology, acetate-CoA ligase homology
C, Superfamily: acyl carrier protein homology <ACLI>
F, 510-950/Domain: acetate-CoA ligase homology <ACLI>
F, 968-1036/Domain: acyl carrier protein homology <ACLI>
F, 1546-1937/Domain: acyl carrier protein homology <ACLI>
F, 2005-2073/Domain: acetate-CoA ligase homology <ACLI>
F, 2005-3013/Domain: acetate-CoA ligase homology <ACLI>
F, 5183-3111/Domain: acyl carrier protein homology <ACLI>
F, 3631-3111/Domain: acetate-CoA ligase homology <ACLI>
F, 3621-4060/Domain: acetate-CoA ligase homology <ACLIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 31; DB 2; Length 6486; 100.0%; Pred. No. 5.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;4078-4146/Domain: acyl carrier protein homology <ACP4>F;465-5104/Domain: acetae-CoA ligase homology <ACL5>F;3122-5190/Domain: acyl carrier protein homology <ACP5-F;5702-6147/Domain: acetate-CoA ligase homology <ACCP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 96.8%; Score 30; DB 2; Best Local Similarity 80.0%; Pred. No. 16; Matches 4; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2664 NYGVH 2668
|||||
208 NYGVH 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: PQ0266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: tycC
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Residues: 1-697 <CON>
A,Cross-references: EMBL:AF000265; NID:g1947147; PID:g1947154; PIDN:AAB52947.1; GSPDB:GN
A,Experimental source: strain Bristol N2; clone C18E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1465 < FNELS.
A; Constant and Con
                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .Species: Homo sapiens (man)
Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
Accession: S43529; S42166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C18E3.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 31; DB 2; Length 1465; 100.0%; Pred. No. 1.2e+02; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 31; DB 2; Length 697; 100.0%; Pred. No. 58; ive 0; Mismatches 0; Indels
                                                                                                                                                                    100.0%; Score 31; DB 2; Length 482; 100.0%; Pred. No. 40; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain Bristol N2; clone clobs
C; Genetics:
A;Gene: CESP:C18E3.7
A;Map position: 1
A;Introns: 12/2; 32/2; 72/1; 219/3; 315/2; 447/3; 666/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: T15179
R;Connell, M.; Maggi, L.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid C18E3.
A;Reference number: Z18304
A;Accession: T15179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                         A,Map position: 1
C,Superfamily: Klebsiella histidine decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Fuerst, D.O. submitted to the EMBL Data Library, October 1992 submitted to the EMBL Data Library, October 1992 A;Reference number: 843529 A;Accession: 843529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule Lype: mRNÅ
A,Residues: 1-101, QR', 104-1465 <VIN>A)Cross references: BMBL:X69089
C;Superfamily: skelemin
C;Keywords: skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165K protein, skeletal muscle - human
                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        NYGVH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 NYGVH 124
                                                                                                                                                                                                                                                                                                                                                 1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NYGVH 5
             A;Gene: F2J6.7
                                                                                                                                                                                                                                                                                                                                                                                                                            139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
843529
                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

Thu Oct 14 09:36:56 2004

1 NYGVH 5 |||:| 31 NYGIH 35

දු දු

Search completed: October 6, 2004, 16:34:45 Job time : 8.26316 secs

This Page Blank (uspto)

```
October 6, 2004, 16:34:15; Search time 31.1404 Seconds (without alignments) 51.669 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

1: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: \cgn2_6/ptodata/2/pubpaa/PCT-TRM PUB.pep:*
3: \cgn2_6/ptodata/2/pubpaa/NCT-TRM PUB.pep:*
4: \cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: \cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
6: \cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
7: \cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
8: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: \cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
13: \cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
14: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
15: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
16: \cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
16: \cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
16: \cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
17: \cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
18: \cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1351062 seqs, 321799191 residues
                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                            US-09-635-974A-2
                                                                                                                                                                                                                                                                                                                                                                                        1 NYGVH 5
                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                              Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 26, Appl Sequence 2, Appli	H	Sequence 1, Appli	231	Sequence 231, App	Sequence 193465,	Sequence 50344, A	Sequence 187665,	Sequence 218420,	Sequence 281738,	Sequence 3, Appli	Sequence 4, Appli	Sequence 115, App	Sequence 116, App
SUMMARIES	US÷09-798-689-26 US÷09-996-9548-2	US-10-374-600-1	US-10-374-531-1	US-09-759-130B-231	US-10-741-790-231	US-10-424-599-193465	US-10-767-701-50344	US-10-424-599-187665	US-10-424-599-218420	US-10-424-599-281738	US-10-435-299-3	US-10-435-299-4	US-10-374-600-115	US-10-374-600-116
	10	12	15	10	16	12	16	12	12	12	12	13	13	12
% Query Match Length DB	, , , ,	Ŋ	Ŋ	19	19	65	68	69	90	93	116	116	119	119
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	31	31	31	31	31	31	31	31	31	31	31	31	31	31
Result No.	177	m	4	ស	9	7	89	σ	10	11	12	13	14	15

1 NYGVH 5

ò

Sequence 117, App	Sequence 118, App	Sequence 119, App	12	9 11	H	11	11	11	12	24	26	27	28	29	30	24	56	27	28	29	30	ω	13	19	ω	13	19	47,	Sequence 47, Appl
2 US-10-374-600-117	US-10-374	2 US-10-374-600-119	US-10-374	US-10-374-	US-10-	US-10-	US-10-374	US-10-374	US-10-	US-10-374	US-10-	US-10-374	US-10-374	US-10-374	US-10-374	5 US-10-374-531-24	US-10-374-53	US-1	US-10-374	US-10-374		US-10-374	US-10-374-		US-10-374-53	5 US-10-374-531-13	1-53	US-09-903-456-47	1 US-10-156-911-47
119 13	9	119 13	9	9	9	9	9	9	9	7	2	2	2	7	7	132 15	2	2	2	2	132 19	8 1	8 1	8	8	138 15	138 19	141 9	141 14
31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0	31 100.0		31 100.0	31 100.0
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
US-09-798-689-26

i Sequence 26, Application US/09798689

i Dublication No. US20030103973A1

GENERAL INFORMATION:

j APPLICANT: Rockwell, Particia

APPLICANT: Rockwell, Particia

APPLICANT: Goldstein, Neil I.

i TITLE 0F INVENTION: Combined With Radiation and Chemotherapy

FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP

CURRENT FILING DATE: 109/09/799,689

CURRENT FILING DATE: 1090-09-22

FRIOR APPLICATION NUMBER: US/09/79,689

CURRENT FILING DATE: 1995-09-22

FRIOR APPLICATION NUMBER: 08/967,113

FRIOR PLING DATE: 1995-06-03

FRIOR APPLICATION NUMBER: 08/706,804

FRIOR PLING DATE: 1995-06-03

FRIOR PLING DATE: 1995-06-03

FRIOR APPLICATION NUMBER: 08/196,041

FRIOR PLING DATE: 1995-06-07

FRIOR APPLICATION NUMBER: 08/196,041

FRIOR PLING DATE: 1994-02-10

NUMBER OF SEQ ID NOS: 41

SSOTTHARE PARENTING DATE: 1994-02-10

NUMBER OF SEQ ID NOS: 41

SSOTTHARE PARENTING DATE: 1994-02-10

NUMBER OF SEQ ID NOS: 41

CREANISM: Mouse

US-09-798-689-26

OUBTY MATCH

BEST Local Similarity 100.0%; Pred. NO. 1.20+06; Indels 0; Indels 0;
```

ô

Gaps

.; 0

us-09-635-974a-2.rapb

```
Sequence 1, Application US/10374531
Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: ImClone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INVENTION: INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

100.0%; Score 31; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DAIA:

PRIOR APPLICATION NUMBER: US/08/973, 065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: ECT/US96/09847
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482, 982
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-374-600-1
REGISTRATION NUMBER: 31,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: S amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                     425-5288
                                                                                                                                                                                    LENGTH: 5 amino acids
                                                                                               TELEFAX: (212) 425-:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-374-531-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                        Sequence 2, Application US/0996954B
; Sequence 2, Application US/0996954B
; Publication No. US20030157104A1
; GENERAL INFORMATION:
    APPLICANT: Maksal, Harlan W
; TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
; TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
; TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
; TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
; TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
; TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
; CURRENT FILING DATE: 09/840,146
; PRIOR FILING DATE: 09/374,028
; PRIOR FILING DATE: 08-13-1999
; PRIOR FILING DATE: 08-14-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
ILREGH: SEQ ID NO 2
ILREGH: SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10374600
Sequence 1, Application US/20030224001A1
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
TIPLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INFIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
COUNTRY: US
ZIATE: New YORK
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 31; DB 10; Length 5; Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: <un>

UNKNOWN>

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens-Rodent Chimera
US-09-996-954B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NYGVH 5
  NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-10-374-600-1
     e
e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

ò g

```
APPLICANT: Wisely Charles R
APPLICANT: Weekey, Charles R
APPLICANT: Weekey, Charles R
APPLICANT: Weekey, Charles R
APPLICANT: Leiby, Kevin Sicolas
APPLICANT: Leiby, Kevin Sicolas
APPLICANT: Leiby, Kevin Sicolas
APPLICANT: Goodeant, Andrew
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: WORL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: DESCRICTC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES: 2003-12-19
FRICA PLING DATE: 2000-01-07
FRICA PLING DATE: 2000-01-07
FRICA PLING DATE: 2000-04-27
FRICA PLING DATE: 2000-04-27
FRICA PLING DATE: 2000-04-27
FRICA PLING DATE: 2000-05-24
FRICA PLING DATE: 2000-06-24
FRICA PLING DATE: 2000-06-30
FRICA PLING DATE: 1999-06-14
FRICA PLING DATE: 1999-06-14
FRICA PLING DATE: 1999-06-14
FRICA PRICATION NUMBER: US 09/596,194
FRICA PLING DATE: 1999-06-10
FRICA PLING DATE: 2000-06-30
FRICA PLING DATE: 309-00-10
FRICA PROFESTION NUMBER: US 09/420,707
FRICA PROFESTION NUMBER: US 09/420,707
FRICA PLING DATE: 309-00-10
FRICA PROFESTION PROFESTION NUMBER: US 09/420,707
F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-424-599-193465

Sequence 193465, Application US/10424599

Publication No. US20040031072A1

SEQUENCE 19365, Application US/10424599

PUBLICANT: La Rosa Thomas J

APPLICANT: La Royalic David K

APPLICANT: Cao Yongwei

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 31; DB 16;
100.0%; Pred. No. 11;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                            APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                      Sequence 231, Application US/10741790
Publication No. US20040121396A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        McCarthy, Sean A
Fraser, Christopher C
Sharp, John D
Barnes, Thomas S
Kirst, Susan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
US-10-741-790-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 NYGVH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NYGVH S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Share, John D
APPLICANT: Share, John D
APPLICANT: Share, John D
APPLICANT: Mackey, Charles R
APPLICANT: Myers, Paul S
APPLICANT: More 
                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 31; DB 10; Length 19; 100.0%; Pred. No. 11; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                         Length 5;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPELICANT: Millennium Pharmaceuticals, Inc.
MCCATHY, Sean A
RPHICANT: Fraser, Christopher C
LPELICANT: Sharp, John D
MOLECULE TYPE: peptide
HYPOTHFILEAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 231, Application US/09759130B Publication No. US20030022279A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Homo sapiens
US-09-759-130B-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 NYGVH 10
                                                                                                                                                                                                                                                                                                                                                                                   1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NYGVH 5
                                                                                                                                                          US-10-374-531-1
```

ó

g ò

```
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100...
Si Conservative
                    Query Match
Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 NYGVH 21
                                                                                                                                                     64 NYGVH 68
                                                                                                                    1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-281738
US-10-424-599-187665
                                                                                                                                                                                                                                     US-10-424-599-218420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 187665, Application US/10424599
Sequence 187665, Application US/10424599
Sublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vancia David K
APPLICANT: Cao Vancyei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 187665
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Wouleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535) B

CURRENT PILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NOS: 63128
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                       100.0%; Score 31; DB 12; Length 65; 100.0%; Pred. No. 38; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 31; DB 16; Length 68; 100.0%; Pred. No. 40; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_140475C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: LIB3478-058-Q6-K1-A9.pep
US-10-767-701-50344
                                                                                                                                                                              OTHER INFORMATION: Clone ID: PAT_MRT3847_16723C.1.pep
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 193465
LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                       ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         41 NYGVH 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 NYGVH 14
                                                                                                                                                                                                                                                                                                                        1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-10-424-599-187665
                                                                                                                                                                                                     US-10-424-599-193465
                                                                                                                                                                                                                                             Query Match
                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
```

```
Sequence 218420, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 218420
LINGTH: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2012.1.

Sequence 102.2013.

Sequence 102.2013.

Publication No. US20040031072A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILIATION DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

FROM THE CONTROL OF SEQ 10 NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 31; DB 12; Length 93; Best Local Similarity 100.0%; Pred. No. 54; Matches 5; Conservative 0; Mismatches 0; Indels
100.0%; Score 31; DB 12; Length 69; 100.0%; Pred. No. 40; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Clone ID: PAT_MRT3847_39261C.1.pep
US-10-424-599-218420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_9642C.1.pep
US-10-424-599-281738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 31; DB 12;
100.0%; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: (1)..(93)
OTHER INFORMATION: unsure at all Xaa locations
```

ö

Gaps

0

Indels

ઠ g

```
RESULT 14
(2-10-374-600-115)
; Sequence 115, Application US/10374600
; Publication No. US20030224001A1
; Publication No. US20030224001A1
; GENERAL INFORMATION:
; APPLICANT: IMCIONE Systems Incorporated, et al.
; TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INTELLING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBELE FORM:

COMPUTER READBELE FORM:

MEDIUM TYPED Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 2-Feb-2003
CLASSIFICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborand A. Somerville
NAME: Deborand A. Somerville
NAME: Deborand A. Somerville
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 116, Application US/10; Publication No. US20030224001A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
· 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 5, Conservative
                                                                                                              31 NYGVH 35
                                                                  1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-374-600-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-374-600-116
Matches
                                                                                                                                d
                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Heavy chain of Humanized 1D10 Ab minus signal sequence US-10-435-299-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 116; 68;
                                                                                                                                                                                                                                                  Sequence 3, Application US/10435299;
Publication No. US2004005278341
GENERAL INPORMATION:
APPLICANT: Weiner George
APPLICANT: Weiner George
APPLICANT: Link, Brian
APPLICANT: Hownit Seg-0176-CNUS04
CURRENT APPLICATION NUMBER: US/10/435,299
CURRENT FILING DATE: 2000-07-18
PRIOR FILING DATE: 1995-03-01
PRIOR FILING DATE: 1995-03-01
PRIOR FILING DATE: 1992-03-27
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 3
LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-LO-425-29-4
Sequence 4, Application US/10435299
Publication No. US204005278341
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Link, Brian
APPLICANT: Link, Brian
APPLICANT: Link, Brian
APPLICANT: Look, Coulso
TILE OF INFORMATION: HUMANIZED ANTIBODIES AGAINST CD3
FILE REFERENCE: 05882-0176-CNUS04
CURRENT APPLICATION NUMBER: US 09/618,380
FRIOR APPLICATION NUMBER: US 09/618,380
FRIOR PLING DATE: 1995-03-01
FRIOR PLING DATE: 1995-03-01
FRIOR FILING PAPEL FRIOR DATE: 1995-03-01
FRIOR FRIOR PAPEL FRIOR DATE: 1995-03-01
FRIOR F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                           14 NYGVH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 NYGVH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NYGVH 5
```

ò

ö

ô

Search completed: October 6, 2004, 17:09:02 Job time : 34.1404 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

6, 2004, 16:24:54; Search time 8.85965 Seconds (without alignments) 29.135 Million cell updates/sec October Run on:

US-09-635-974A-2 31 1 NYGVH 5 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

389414 segs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

ssued_Patents_AA:*
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 3, Appli Sequence 4, Appli Sequence 14, Appli Sequence 47, Appli Sequence 20, Appli 5340, Ap 2, Appli Sequence 27, Appl Patent No. 5455030 Patent No. 5455030 Sequence 64, Appl Sequence 6, Appli App] Description Sequence Seq Sequence Sequence 1 Sequence Sequence Sequence Sequence US-08-397-411-6 US-08-397-411-7 US-09-134-000C-5340 US-08-483-745A-14 US-09-903-456-47 US-09-145-828A-20 US-09-903-456-27 5455030-13 US-08-211-430-2 US-08-761-136-1 US-09-576-967-1 US-08-652-558-39 US-09-240-274-8 US-09-240-274-16 US-09-240-274-147 US-09-240-274-148 5455030-15 US-09-903-456-64 -09-240-274-12 SUMMARIES Query Match Length Result Š.

Sequence 75, Appl Sequence 4950, Ap	equence 68,	sequence 2, Appli Sequence 9, Appli	o,	o,	4	375	7		798		Sequence 42, Appl	53,	Sequence 18, Appl	Sequence 24, Appl	5242
US-09-472-087-75 US-09-328-352-4950	09-456-090	US-U8-48U-753-2 US-09-041-889-9	US-08-837-058-9	US-09-417-264-9	US-08-480-753-4	US-09-134-001C-3752	US-09-472-087-2	US-09-472-087-66	US-09-489-039A-7985	US-09-328-352-5717	US-09-724-864-42	US-09-903-456-53	US-09-145-828A-18	US-09-903-456-24	US-09-134-000C-5242
4 4	47' (7 M	ო	4	~	4	4	4	4	4	4	4	4	4	4
166	225	233	233	233	244	347	464	464	498	701	228	271	272	272	319
90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	87.1	87.1	87.1	87.1	87.1
28 28	9 69	69 G 77 V	28	28	58	28	28	28	28	28	27	27	27	27	27
28	30	1 Z 1 M	33	34		36		38		40	41	42	43	44	45

ALIGNMENTS

```
RESULT 1

US-08-397-411-3

Sequence 3, Application US/08397411

Sequence 3, Application US/08397411

Setent No. 612994

GENERAL INFORMATION:

APPLICANT: Wedner, George
APPLICANT: Link, Brian

APPLICANT: Link, Brian

TITLE OF INVENTION: Bispecific Antibody Effective to Treat

TITLE OF INVENTION: B-Cell Lymphoma and Cell Line

TITLE OF INVENTION: B-Cell Lymphoma and Cell Line

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTE: 74105
COMPUTE: 74105
COMPUTE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TEM PC compatible
COPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR.1995
CLASSIFICATION NUMBER: US/08/397,411
PRICATION NUMBER: US/08/397,411
PRICATION NUMBER: US/08/397,411
APPLICATION NUMBER: US/08/397,411
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 30,223
REGISTRATION INFORMATION:
TELEPHONE: 415-326-2407
TELEPHONE: 415-326-2407
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
LENGTH: 116 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-08-397-411-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105
```

ó

Gaps

. 0

100.0%; Score 31; DB 3; Length 116; 100.0%; Pred. No. 24; tive 0; Mismatches 0; Indels

Conservative

Query Match Best Local Similarity Matches 5; Conserv

Sequence

8 d

```
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/483,749A
FILING DATE: 07-UW-1995
CLASSIFICATION: 536
ATTOWNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET UNMER: 36,914
REGISCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (510) 601-2585
INTELLECTUAL PROPERTY - R440, PO BOX 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                  ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-903-456-47

Sequence 47, Application US/09903456

Patent No. 6677145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 119 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-483-749A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                     EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 NYGVH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NYGVH 5
                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 47
LENGTH: 141
                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08483749A

Patent No. 6054561

CENERL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               Sequence 4, Application US/08397411

Patent No. 6129914
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weinger, George
APPLICANT: Link, Brian
APPLICANT: Tso, J. vun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B. Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 31; DB 3; Length 116; 100.0%; Pred. No. 24; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
21P: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  011823-004901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 01-MAR-1995
CLASASIFICATION: 424
PRIOR APPLICATION DATA: 07/859,583
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, william M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-24M0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-397-411-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 NYGVH 35
                                                                                                               31 NYGVH 35
                                                    1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-08-483-749A-14
                                                                                                                                                                                                                           RESULT 2
US-08-397-411-4
```

÷

```
Gaps
                                                      Gaps
                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 31; DB 4; Length 141; 100.0%; Pred. No. 29; 0; Indels tive 0; Mismatches 0; Indels
100.0%; Score 31; DB 3; Length 119; 100.0%; Pred. No. 24;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COTHER INFORMATION: (141)...(141); OTHER INFORMATION: Xaa = Unknown or Other at position 141 US-09-903-456-47
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: AMbort Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Monardi Bun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELDONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FASESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 5; Conservative
```

рþ

o O

ઠ g

```
RESULT 7
5455030-13
; PATENT LADNER, ROBERT C., BIRD, ROBERT E., HARDWAN, KARL
TILLE OF INVENTION: IMMUNOTHERAPHY USING SINGLE CHAIN
; POLYBEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; PRIOR DATE: 1-RPE-1933
; PRIOR APPLICATION DATA:
; APPLICATION DATA:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 25, 29, 617
; FILING DATE: 15-APR-1999
; FILING DATE: 19-APR-1989
; FILING DATE: 01-SEP-1987
; FILING DATE: 01-SEP-1986
; FILING DATE: 01-SEP-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
5455030-15
5 PATEN NO. 5455030

**APPLICANT: LADNER, ROBERT C.;BIRD, ROBERT E.;HARDMAN, KARL
TITLE OF INVENTION: IMMUNOTHERAPHY USING SINGLE CHAIN
FOLYPEPTIDE BINDING MOLECULES
**NUMBER OF SEQUENCES: 24

**NUMBER OF SEGUENCES: 24

**CURRENT APPLICATION DATA:
**APPLICATION NUMBER: US/08/40,440

**FILING DATE: 1-ARR-1993

**PRICATION NUMBER: 512,910

**FILING DATE: 15-ARR-1990

**APPLICATION NUMBER: 92,110

**FILING DATE: 19-ARN-1989

**APPLICATION NUMBER: 92,110

**FILING DATE: 02-SEP-1987

**FILING DATE: 01-SEP-1986

**FILING DATE: 01-SEP-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 31; DB 6; Length 239; 100.0%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 31; DB 6; Length 242; Best Local Similarity 100.0%; Pred. No. 50; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 64, Application US/09903456
Patent No. 6677145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 NYGVH 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 NYGVH 157
NYGVH 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 31; DB 4; Length 147; 100.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mikerji, Pradig
APPLICANT: Mikerji, Pradig
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Thurmond, Jennifer
APPLICANT: Thurmond, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/09903456
; Bacent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbort Laboratories
; APPLICANT: Beneria, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; PRERERENCE: 2001-07-11
; TITLE OF INVENTION: 2LONGASE GENES AND USES THEREOF
; TITLE OF INVENTION WUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
                                                                                                                                                                                                                                            3-09-145-828A-20
Sequence 20, Application US/09145828A
Patent No. 6403349
```

Query Match 100. Best Local Similarity 100. Matches 5; Conservative

1 NYGVH 5

ò

TYPE: PRT ORGANISM: Homo sapiens

US-09-145-828A-20

ö

TYPE: PRT
CORGANISM: Homo sapiens
US-09-903-456-27

```
RESULT 12
US-09-134-000C-5340
; Sequence 5340, Application US/09134000C
                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 446 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
    STRANDEDNESS: single
                        TOPOLOGY: linear MOLECULE TYPE: peptide US-08-397-411-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: sir
                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 NYGVH 35
                                                                                                                                                                                                                                                           31 NYGVH 35
                                                                                                                                                                                                              1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-397-411-7
                                                                                                                                                                                                                                                                                                                                                         US-08-397-411-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-39-1411-0

Patent No. 6129914

FARERIA INFORMATION:

GENERAL INFORMATION:

APPLICANT: Weiner, George

APPLICANT: Gingrich, Roger

APPLICANT: TSO, Yun

APPLICANT: TSO, Yun

TITLE OF INVENTION: Bispecific Antibody Effective to Treat

TITLE OF INVENTION: B-Cell Lymphoma and Cell Line

NUMBER OF SEQUENCE: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STREET: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 31; DB 4; Length 265; 100.0%; Pred. No. 55; 0; Indels tive 0; Mismatches 0; Indels
APPLICANT: Mukerji, Pradip
APPLICANT: Lecnard, Amanda Eun-Yeong
APPLICANT: Lecnard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVEXTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-3
PRIOR FILING DATE: 1999-08-3
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIPICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 011823-004901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Smith, William M. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity luv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-903-456-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 NYGVH 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NYGVH S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 64
LENGTH: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 31; DB 3; Length 446; 100.0%; Pred. No. 93; ive 0; Mismatches 0; Indels
DB 3; Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
  100.0%; Score 31; DB 100.0%; Pred. No. 57;
                           Mismatches
                                                                                                                                                                                                                                                                                                                                                 STATE:
COUNTY:
USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver:
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
TING DATE: 01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   011823-004901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTONNE AGENT INFORMATION:
NAME: Smith, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 0118;
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2402
INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS:
```

```
SOUSSI-YANTICOCTAS, NADIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-576-967-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-761-136-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08211430

Patent No. 5763166

APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
COMPUTER: PARENCES:
COMPUTER: BEADABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: BARENCES:
COMPUTER: BARENCES:
COMPUTER: BARENCES:
COMPUTER: COMPUTER: COMPATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/211,430
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER: COMPUTER: COMPATION COMPATION FOR SEQ ID NO:
CURRENT APPLICATION COMPATION COMPATION FOR SEQ ID NO:
COMPUTER: COMPATI
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 032796-032
CURRENT APPLICATION NUMBER: US 60/059,778
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 505,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
96.8%; Score 30; DB 1; Length 680;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 4; Length 505
Pred. No. 1.7e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08761136
Patent No. 6121231
GENERAL INFORMATION:
APPLICANT: PETIT, CHRISTINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CELL LINE: foetal brain cell US-08-211-430-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.8%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 680 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||:|
195 NYGIH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 NYGIH 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-134-000C-5340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-211-430-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-761-136-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
APPLICANT: PETIT, CHRISTINE
SOUSSI-YANTICOCTAS, NADIA
HARDELIN, JEAN-PIERRE
SARAILH, CATHERINE
ROUGON, GENEVIEVE
LEGOUIS, RENAUD
ARDOUIN, OLIVIER
MAZIE, JEAN-CLAUDE
TITLE OF INVENTION: USE OF KAL PROTEIN AND TREATMENT WITH
AND NEURAL INJURY
AND NEURAL INJURY
                                                                APPLICANT: ROUGON, GENEVIEWER
APPLICANT: REGOUIS, RENAUD
APPLICANT: AROUND, OLIVIER
APPLICANT: AROUND, OLIVIER
APPLICANT: MAZIE, JEAN-CLAUDE
TITLE OF INVENTION: USE OF KAL PROTEIN AND TREATMENT WITH
TITLE OF INVENTION: THE KAL PROTEIN IN TREATMENT OF RETINAL, NEUROMAL
TITLE OF INVENTION: AND NEURAL INJURY
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 3; Leus...
Pred. No. 2.38+02;
O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-DEC.1996
FILING DATE: 06-DEC.1996
FILING DATE: 06-DEC.1996
FILING PATE OF TOWNER: FOR THE PARE: FOR THE PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
HARDELIN, JEAN-PIERRE
SARAILH, CATHERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/09576967; Patent No. 6548475; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 NYGIH 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
```

us-09-635-974a-2.rai

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
CONFUTE: VA
COUNTYER: VGA
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA: 14-MAY-200
FILING DATE: 24-MAY-200
FILING DATE: 34-MAY-200
FILING DATE: 30-MAY-200
FILING TARACTERITON:
FROMMUNICATION INFORMATION:
FILING TOWN OF SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FILING TOWN OF SEQ ID NO: 1:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
MOLECULE TYPE: AND ACID
FILING THE DATE: 30-MAY-200
FILING THE PROBLEM OF SEQ ID NO: 1:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQ ID NO: 1:
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQ ID NO: 1:
MOLECULE TYPE: DATE: 30-MAY-200
FILING THE PROBLEM OF SEQ ID NO: 1:
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQ ID NO: 1:
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQ ID NO: 1:
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQ ID NO: 1:
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQ ID NO: 1:
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQ ID NO: 1:
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQUENCE DESCRIPTION: SEQ ID NO: 1:

MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQUENCE DESCRIPTION: 2:3-402;
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQUENCE DESCRIPTION: 2:3-402;
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQUENCE DESCRIPTION: 2:3-402;
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQUENCE DESCRIPTION: 2:3-402;
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SECUENCE DESCRIPTION: 2:3-402;
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQUENCE DESCRIPTION: 3-3-402;
MOLECULE TYPE: AND ACID
FILING THE PROBLEM OF SEQUENCE DESCRIPTION: 3-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NYGVH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
```

Search completed: October 6, 2004, 16:36:30 Job time: 9.85965 secs

224 NYGIH 228

DP

us-09-635-974a-10.rpr

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

October 6, 2004, 16:23:59 ; Search time 6.31579 Seconds (without alignments) 91.382 Million cell updates/sec Run on:

US-09-635-974A-10 25 1 ASESIS 6 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

, , , , , , , , , , , , , , , , , , ,		g light chain V	g kappa chain V	g kappa chain V	Ig kappa chain pre	Ig kappa chain pre	pothetical pr	pgal protein - Asp	coiled-coil protei	pumilio family pro	phosphatidylinosit	microtubule-vesicl	restin - human	hypothetical prote	hypothetical prote		E	threonyl-tRNA synt	ger	err		probable transcrip	bride of sevenless	fic meta	ble	riae-asso	CDA peptide synthe	hetical	ical	hypothetical prote
Ę	Q.T.	PH1082	m	C30502	KVMSL7	PN0445	E90552	S17980	T37740	T50143	JC4889	A43336	\$22695	F84169	T19485	T13299	849790	A81656	9	ď	0	4.	ñ	503	Н.	ŝ		156	246	385
9	9 ;	7	Н	N	-	7	N	~	7	0	~	N	N	N	~	~	~	~	~	7	7	7	~	0	0	۲۷	~	~	7	7
7	nengen	87	92	0	ч	N	4	ø	4	m	18	σ,	42	0	4	4	σ	3	æ	œ	O)	S	σ	53	m	57	3670	Н	4	_
Query	ממרכיו	ö	00	00	00	00	ö	00	ö	00	ö	ö	ö	ů.	Ġ	ú	ů	ů.	ů	Ġ	è.	ů.	ú	ė	ů	ů.	96.0	ď	'n	ď
0	2000																										24			
Result No		н	7	m	4	ហ	9	7	00	σı	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	chaperone protein		pilQ protein - Nei	pilus secretin NMA	suppressor of sabl	hypothetical prote	pothetical	Ig light chain V r	kappa	chain	chain	Ig kappa chain V r	chain	Ig kappa chain V r
S67571	AB0824	A37051	570838	A81985	T13855	T30037	T24490	PH1080	S78488	516827	534086	S16840	534084	S34083
00	10	0	7	7	7	Ŋ	7	7	N	N	~	(1	~	04
583 584	616	711	720	761	1473	1539	2251	69	86	98	86	86	87	87
92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0
23	23	23	23	23	23	23	23	22	22	22	22	22	22	22
30	35	33	34	35	36	37	38	9,9	40	41	42	43	44	4.5

ALIGNMENTS

	RESULT 1	
	PH1082	
_	Ig ligh	Ig light chain V region (clone 165.54) - mouse (fragment)
	C, Speci	C;Species: Mus musculus (house mouse)
	C;Date:	C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
	C;Acces	C, Accession: PH1082
	R;Tillm	an, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
	J. Exp.	J. Exp. Med. 176, 761-779, 1992
	A; Title	A, Title: Both 19M and 19G anti-DNA antibodies are the products of clonally selective
	A;Refer	A; Reference number: PH0971; MUID:92381444; PMID:1512540
_	A; Acces	A; Accession: PH1082
_	A;Statu	A;Status: nucleic acid sequence not shown
	A; Molecu	A; Molecule type: mRNA
	A, Resid	A;Residues: 1-87 <til></til>
_	A; Exper:	A,Experimental source: B cell, strain [NZB x NZW]F1
	C; Super:	C, Superfamily: immunoglobulin V region; immunoglobulin homology
	C; Keywo:	C; Keywords: immunoglobulin
	F;6-80/	F;6-80/Domain: immunoglobulin homology < IMM>
	į	
	Cuery Post,	Query Match 100.0%; Score 25; DB 2; Dength 8/;
	Matchod	BEST LOCAL SIMILATILY 100.0%; FIEGG. NO. 0.2; N. M. STATANCE C. ORDERATE OF TAGGER O. 123
	HIDO BIL	סי כסוים בי שרבי כי הודמוושרכוים כי דוומבים כי פסקם
	<i>ਨ</i>	1 ASESIS 6
	Db	41 ASBSIS 46
_	1	

m

41 g

Notes to the chain V region (3381) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: A01953
R;Margolies, M.N.; Cannon III, L.E.; Strosberg, A.D.; Haber, E.
Proc. Natl. Acad. Sci. US.A. 72, 2180-1284, 1975
A;Title: Diversity of light chain variable region sequences among rabbit antibodies elic A;Reference number: A93799; MUID:75176905; PMID:1094456
A;Accession: A01953
A;Accession: A01953
A;Accession: A01953
A;Residues: 1-92 cMAR>
C;Comment: This chain was obtained from antibody to type III pneumococci and was isolate C;Comment: This chain heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin vegion; immunoglobulin homology ciMM>
F;23-88/Disulfide bonds: #status predicted

Gaps ö Query Match
100.0%; Score 25; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 6; Conservative 0; Mismatches 0; Indels

ö

```
A;Introns: 76/3; 216/3
C;Superfamily: polygalacturonase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pgal protein - Aspergillus niger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                      A;Accession: PN0445
A;Molecule type: mRNA
A;Residues: 1-128 <KAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-248 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-368 <BUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ASESIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 ASESIS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: MYPU 3250
A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S17980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A;Residues: 1-115 <PEC>
A;Residues: 1-115 <PEC>
A;Cross-references: GB:V01564; GB:J00574; NID:g51718; PIDN:CAA24884.1; PID:g758153
A;Note: the sequence was determined from the germline gene
A;Note: there appear to be two possible splice junctions at the 3' end of the intron; th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region, immunoglobulin homology
C;Superfamily: immunoglobulin V region, immunoglobulin homology
C;Keywords: heterotetramer
F;1-20/Domain: signal sequence #status predicted <SIG>
F;2-110/Pomain: immunoglobulin V region (L7) #status predicted <WAT>
F;36-110/Domain: immunoglobulin homology <IMM>
F;36-110/Domain: immunoglobulin pomology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain precursor V region (L7) - mouse (5)pecies: Mus musculus (house mouse) (5)bate: IB-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 22-Jun-1999 (5)bate: IB-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 22-Jun-1999 (5)batession: A01925 (5)batession: A01925 (5)batession: A01925 (5)batession: A)bates (5)batession: A)bates (5)bates (5)bates
                                                                                                                                                                                           RESULT 3
C30502
C30502
Gy Appear Chain V region (D444) - mouse
C; Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C;Accession: 030502
C;Accession: 030502
C; Musculus Day, Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 17A;Cession: 030502
A;Steference number: A30502; MUID:88315787; PMID:2457627
A;Stetus: preliminary
A;Mccession: C30502
A;Stetus: preliminary
A;Mccession: C30502
A;Stetus: preliminary
A;Mccession: C30502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g197072 C;Superfamily: immunoglobulin vegion; immunoglobulin homology C;Keyworda: heterotetramer; immunoglobulin P;166-90/Domain: immunoglobulin homology <IVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 25; DB 2; Length 108; Best Local Similarity 100.0%; Pred. No. 10; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 1; Length 115; 100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
PN0445
Ig kappa chain precursor V-I region - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                          ASESIS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-108 < EIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASESIS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASESIS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASESIS 6
φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ASESIS 6
ASESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 17/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

```
hypothetical protein MYPU 3250 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: E90552
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Rieference mumber: A99512; MUD:21267165; PMID:11353084
A;Accession: E90552
C,Species: Homo sapiens (man)
C,Species: Homo sapiens (man)
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C,Accession: PN0445
R,Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
R,Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
A,Title: 321-328, 1992
A,Title: Ageneral method for chimerization of monoclonal antibodies by inverse polymeras A,Reference number: PN0444; MUID:93138402; PMID:1339379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CiSpecies: Aspergillus niger
CiActe. 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
CiAccession: 817980
R;Bussink, H.J.D.; Brouwer, K.B.; de Graaff, L.H.; Kester, H.C.M.; Visser, J.
Curr. Genet. 20, 301-307, 1991
A;Title: Identification and characterization of a second polygalacturonase gene of Asperg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AL445566; PID:g14089739; PIDN:CAC13498.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                    A)Cross-references: GB:L02347
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-10/Domain: signal sequence #status predicted <SIG>
F;11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
F;26-100/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: EMBL:X58892; NID:g2382; PIDN:CAA41693.1; PID:g2383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 2; Length 248; 100.0%; Pred. No. 27; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 2; Length 128; 100.0%; Pred. No. 13; ive 0; Mismatches 0; Indels
```

ે 셤

```
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Nov-1999
C;Accession: $22669; $18983
C;Accession: $22669; $18983
ER;Bilbe, G;, Delabie, J; Brueggen, J; Richener, H.; Asselbergs, F.A.M.; Cerletti, N.;
EMBO J. 11, 2103-2113, 1992
EMBO J. 11, 2103-2113, 1992
A;Atlle: Restin: a novel intermediate filament-associated protein highly expressed in th A;Accession: $22695; WUID:92289675; PMID:1600942
Riprover, A.L.; Pesesse, X.; De Smedt, F.; Woscholski, R.; Parker, P.; Erneux, C. Biochem. Blochem. Blochem. 225, 243-249, 1996
Biochem. Blochys. Res. Commun. 225, 243-249, 1996
Biochem. Blochys. Res. Commun. 225, 243-249, 1996
A;Title: Cloning and expression of a human placenta inositol 1,3,4,5-tetrakisphosphate, A;Accession: UC4889; MUID:96332436; PMID:8769125
A;Contents: placenta
A;Accession: UC4889
A;Accession: PC4187
A;Accession: PC4187
A;Accession: PC4187
A;Accession: PC4187
A;Accession: UC4889

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A43336
microtubule-vesicle linker CLIP-170 - human
microtubule-vesicle linker CLIP-170 - human
G;Species: Homo sapiens (man)
G;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
G;Accession: A43336
A;Pierre, P; Scheel, J; Rickard, J.E.; Kreis, T.E.
A;Pierre, P; Scheel, J; Rickard, J.E.; Kreis, T.E.
A;Filte: CLIP-170 links endocytic vesicles to microtubules.
A;Reference number: A43336; MUID:92405160; PMID:1356075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1392 <PIE>
A;Cross-references: GB:M97501; NID:g180621; PIDN:AAA35693.1; PID:g180622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: mRNA
A,Residues: 1-1427 <BLL>
A,Cross-references: EMBL:X64838; NID:g35998; PIDN:CAA46050.1; PID:g35999
C,Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25, DB 2; Length 1188; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 25; DB 2; Length 1392; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cirefronds: phosphoric monoester hydrolase
F;5-101/Domain: SH2 homology <5H2>
F;380/Binding site: substrate (Arg) #status predicted
F;671/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 ASESIS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 ASESIS 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restin - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Accession: T37740

R;Rieger, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A;Reference number: 221743
A;Reference number: 221743
A;Accession: T37740
A;Reference number: L21743
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-649 <RIE>
A;Residues: 1-649 <RIE>
A;Cross-references: EMBL:AL035248; PIDN:CAA22848.1; GSPDB:GN00066; SPDB:SPAC167.03c
A;Experimental source: strain 972h-; cosmid c167
A;Gnetics:
A;Gene: SPDB:SPAC167.03c
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T50143
R;Hamiin, N.; Churcher, C.M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, November 1999
A;Reference number: 225043
A;Accession: T50143
A;Accession: T50143
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolcoule type: DNA
A;Rolcoule type: DNA
A;Residues: 1-732 <HAM>A;Residues: 1-732 <HAM>A;Residues: 1-732 <HAM>A;Coss-references: EMBL:AL132798; PIDN:CAB60694.1; GSPDB:GN00066; SPDB:SPAC222.02c
A;Experimental source: strain 972h(-); cosmid c222
                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pumilio family protein [imported] - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase (EC 3.1.3.-) - human N,Alternate names: hppl.Nsphosphatase (5,5pecies: Homo sapiens (man) (C,Species: Homo sapiens (man) (c,Species: 10-Sep-1996 #sequence_revision 18-Oct-1996 #text_change 05-Nov-1999
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
    Query Match
100.0%; Score 25; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 2; Length 732; larity 100.0%; Pred. No. 92; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 2; Length 649; 100.0%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C'Genetics:
AjGene: SPAC1687.22c; SPDB:SPAC222.02c
AjMap position: 1
A;Introns: 656/2; 711/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 ASESIS 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 ASESIS 16
                                                                                                                                                                      1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASESIS
```

RESULT 9

ð

ò g ö

; 0

ö

Gaps

. 0

```
Match 16.0%; Score 24; DB 2; Length 443; Local Similarity 83.3%; Pred. No. 18+02; less 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: October Job time: 9.31579 secs
                                                                                                                                                                                                                                                                                                                                                                                                    225 ASESVS 230
                                                                                                                                                                                                                                                                                                                                                          1 ASESIS 6
                                                                                                                                                                                                                                                                  Query Match
Best Local S:
Matches 5,
                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                         hypothetical protein Vng0091c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
S;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-304 <STO>
A;Cross-references: GB:AE004437; NID:g10579742; PIDN:AAG18722.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG0091C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the BMBi Data Library, October 1995
A;Reference number: Z19129
A;Reference number: Z19129
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-349 <WILD
A;Residues: 1-349 <WILD
A;Residues: 1-349 <WILD
C;Genetics: Clone CZ6D10
C;Genetics: Clone CZ6D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19485
R;Sims, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable helicase - Streptococcus phage phi-O1205
C;Species: Streptococcus phage phi-O1205
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                               ô
100.0%; Score 25; DB 2; Length 1427; 100.0%; Pred. No. 2e+02; ative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
T19485
hypothetical protein Ć26D10.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 2;
Pred. No. 78;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 2
Pred. No. 66;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3
Frac 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: CESP:C26D10.3
A,Map position: 2
A,Introns: 47/3; 197/1; 277/3
                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 ASESVS 234
                                                                                                                                      192 ASESIS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 ASESVS 217
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ASESIS 6
                                                                                         1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
T13299
                                                 Matches
                                                                                                                                                                                                     RESULT 13
                                                                                              ò
                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
C; Accession: T13299
R; Stanley, E.; Fitzgerald, G.F.; Le Marrec, C.; Fayard, B.; van Sinderen, D.
Microbiology 143, 3417-3429, 1997
A; Title: Sequence analysis and characterization of phi 01205, a temperate bacteriophage
A; Reference number: 217654; MUID: 98048466; PMID: 9387220
A; A; Status: translated from GB/EMBL/DDBJ
A; Residus: translated from GB/EMBL/DDBJ
A; Residues: 1-443 < STA>
A; Residues: 1-443 < STA>
A; Residues: 1-443 < STA>
A; Experimental source: host Streptococcus thermophilus strain CNRZ1205
```

.; 0

Gaps

.. 0

6, 2004, 16:34:54

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

6, 2004, 16:20:48 ; Search time 75.7895 Seconds
 (without alignments)
55.921 Million cell updates/sec October Run on:

US-09-635-974A-4 88 1 VIWSGGNTDYNTPFT 15 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:*
11: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp201s:*
6: geneseqp2003as:*
7: geneseqp2003as:*
8: geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aaw08940 CDR2 from	N	m	ŭ	Aaw08939 CDR2 from		Aaw08950 Heavy cha	Aaw08952 Heavy cha	Aaw08951 Heavy cha	4 Heavy			Aaw08942 Heavy cha	Aaw05133 Single ch	Aaw05135 scFv (225)	8	9 scFv2(FR	Aaw05141 scFv2 (FRP	Aae17798 E. coli m	Aae17793 Escherich	56 A	Aau72848 Anti-NKG2	43	Aar25728 Humanised	Aab69676 Humanised
OI	AAW08940	AAY59312	AAB37953	AAU77785	AAW08939	AAW08953	AAW08950	AAW08952	AAW08951	AAW08954	AAW08947	AAW08944	AAW08942	AAW05133	AAW05135	AAW05140	AAW05139	AAW05141	AAE17798	AAE17793	AAU72856	AAU72848	ADD25438	AAR25728	AAB69676
DB	10	m	4	'n	~	(7	7	(7)	~	N	7	N	~	7	7	7	7	~	ស	Ŋ	Ŋ	Ŋ	,	7	4
Length	16	16	16	16	18	Н	119	н	\vdash	н	138	m	3	4	tO	g	σı	CA	16	114	16	16	ч	119	
% Query Match	100.0	100.0	00	100.0	100.0	100.0	100.0	00	100.0	100.0	100.0	8	100.0	100.0	100.0	0	ö			o,	73.9			۳,	
Score	88	88	88	88	88	88	88	88	88	88	88	88	88	88	88	88	88	88	70	70	65	65	65	65	65
Result No.	-	7	m	4	'n	w	7	α	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aab69675 Murine mi	Aab69660 Human Lay	Aau72846 Anti-NKG2	Aau72854 Anti-NKG2	Aar06355 Peptide c	Aab69656 Murine mi	Aar56235 h66-118/h	Aar56236 166-111/1	Aar14704 Vl-Lab-Vh	Aar14789 Vl-Lab-Vh	Aar14695 Vl-Lab-Vh	Aar14696 Vl-Lab-Vh	Aar14697 Vl-Lab-Vh	Aar14694 Vl-Lab-Vh	Aar14702 Vh-Lab-Vl	Aar14703 Vh-Lab-Vl	Aar14699 Vh-Lab-Vl	Aar14700 Vh-Lab-Vl	Aar14701 Vh-Lab-Vl	Aar15690 Vl-Lab-Vh
AAB69675	AAB69660	AAU72846	AAU72854	AAR06355	AAB69656	AAR56235	AAR56236	AAR14704	AAR14789	AAR14695	AAR14696	AAR14697	AAR14694	AAR14702	AAR14703	AAR14699	AAR14700	AAR14701	. AAR15690
4	4	വ	'n	N	4	~	~	~	N	7	7	7	7	7	7	7	7	7	7
119	119	120	120	127	138	219	223	228	228	235	235	235	235	236	236	236	236	236	236
73.9						73.9		٠.		73.9				73.9					
														65					
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAW08940 standard; peptide; 16 AA. 18-SEP-1997 (first entry) AAW08940; RESULT 1 AAW08940

CDR2 from heavy chain variable region of reshaped H225 antibody.

Complementarity determining region 2; CDR2; heavy chain; variable region; reshaped; human; monoclonal; antibody; H225; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate.

Homo sapiens.

WO9640210-A1.

19-DEC-1996,

96WO-US009847. 07-JUN-1996;

95US-00482982. 95US-00573289. 07-JUN-1995; 15-DEC-1995; (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.

Saldanha JW; Goldstein NI, Giorgio NA, Jones ST,

WPI; 1997-051897/05.

Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.

Claim 1; Page 83; 112pp; English.

The present peptide is the complementarity determining region 2 (CDR2) from the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, which is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in manas, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor

Sequence 16 AA;

AAB37953 standard; protein; 16 AA.

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the hypervariable region CDR2 (complementarity determining region 2) of the heavy chain of a single chain antibody derived from the murine antibody 255. The invention relates to a method for inhibiting the growth of tumours in human patients by treating with an effective amount of a combination of radiation and a non-radiolabelled protein receptor tyrosine kinase (PRTK) inhibitor, the overexpression of which can lead to tumourigenesis. The method can be used in the treatment of tumours of e.g. breast, lung, colon, kidney, bladder, head and neck, one of print makes the administration of a snitable antibody to
                                                                                                                                                                                                                                                                                                         Hypervariable region, complementarity determining region, CDR, tumour; single chain antibody, growth inhibitor; human, tumourigenesis; therapy, protein receptor tyrosine kinase, heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of human tumors, using a combination of radiation and a non-radiolabeled protein receptor tyrosine kinase inhibitor.
                                             Gaps
                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the patient makes the tumour more susceptible to radiotherapy
           100.0%; Score 88; DB 2; Length 16; 100.0%; Pred. No. 2.9e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 88; DB 3; I
100.0%; Pred. No. 2.9e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buchsbaum DJ;
                                                                                                                                                                                                                                                                              Heavy chain hypervariable region, CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 14; 31pp; English.
                                                                                                                                                                                    AAY59312 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robert F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US010741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0085613P.
98US-00206138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00079612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMCL-) IMCLONE SYSTEMS INC. (UABR-) UAB RES FOUND.
                                                                           1 VIWSGGNTDYNTPFT 15
                                                                                                       VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                              07-MAR-2000 (first entry)
Query Match
Best Local Similarity luv..
Best Local Similarity luv..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saleh MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-062440/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ48626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-1998;
15-MAY-1998;
07-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                     WO9960023-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    25-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waksal HW,
                                                                                                                                                                                                                   AAY59312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                           Mus sp.
                                                                                                                                                    ò
                                                                                                        유
```

```
This invention relates to a method for inhibiting the growth of factor receptor (GGFR) in human parients. The method involves treating the patient with a combination of EGFR/human EGF-1 (HER1) antegonist, optionally with a chemotherapeutic agent or radiation. The antegonist can be for example a chimeric anti-EGFR monoclonal antibody, C25s. The EGFR/HER1 antagonist is useful for inhibiting the growth of refractory tumours such as tumours of breast, heart, lung, small intestine, colon, spleen, kidney, bladder, head and nack, ovary, prostate, brain, pancreas, skin, bone, bone marrow, blood, thymus, uterus, testicles, cervix and liver, preferably squamous cell carcinomas. The present sequence represents the heavy chain variable region complementarity determining region 2 amino acid sequence of the chimeric anti-EGFR monoclonal antibody C225 which is used in an example illustrating the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epidermal growth factor receptor/human epidermal growth factor receptor-1 antagonist for inhibiting the growth of refractory tumors.
                                                                                                                            Refractory tumour growth inhibition, epidermal growth factor receptor; EGFR antagonist; cancer; squamous cell carcinoma; anti-EGFR antibody; complementarity determining region; CDR.
                                                                                            Anti-EGFR monoclonal antibody H chain V region CDR2 peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse heavy chain hypervariable region (CDR2) of 225 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 88; DB 4; Length 16; 1 Similarity 100.0%; Pred. No. 2.9e-07; 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 13, 31pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU77785 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                              99US-00312284.
99US-00374028.
                                                                                                                                                                                                                                                                                             01-MAY-2000; 2000WO-US011756.
                                                                                                                                                                                                                                                                                                                                                                                 (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VIWSGGNTDYNTPFT 15
                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-016160/02.
N-PSDB; AAC83236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16 AA;
                                                                                                                                                                                                                                WO200069459-A1.
                                                                                                                                                                                                                                                                                                                              14-MAY-1999;
13-AUG-1999;
                                                                12-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-2002
                                                                                                                                                                                                                                                               23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                 Waksal HW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nvention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU77785;
                               AAB37953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AXAXEXEX
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

0;

Mouse; heavy chain; antibody; hyperproliferative disease;

ö

Gaps · 0

0; Indels

VIWSGGNTDYNTPFT 15

g

ઠે

RESULT 3 AAB37953

1 VIWSGGNTDYNTPFT 15

Conservative

```
This invention relates to a novel method for treating a mammal with hyperproliferative disease stimulated by a ligand of a member of the epidermal growth factor (EGF) family of receptors. The method involves administering an antibody or a defective receptor that is an antagonist of a member of the EGF receptor family, or a combination of the antagonist and phototherapy, chemotherapeutic agent or radiation herapy. The antibody used in the method of the invention acts as an epidermal growth factor receptor (EGFR) antagonist by inhibiting EGFR /HERI phosphorylation. The method of the invention is useful for treating a mammal with hyperproliferative disease such as psoriasis, actinic stimulated by a ligand of a member of the EGF family of receptor. This sequence represents the mutine anti-EGF 255 antibody heavy chain (VH) hypervariable region (CDR2) used as an inhibitor of EGFR in the method of
                                                                                                                                                                                                                                                                                                                                                                                Treating a mammal with hyperproliferative disease especially psoriasis, stimulated by ligand of member of epidermal growth factor family of receptors, by administering antagonist of the receptor.
epidermal growth factor; EGF; psoriasis; actinic keratosis; seborrheic keratosis; warts; keloid scars; eczema; 255 antibody; hypervariable region; CDR2; EGFR inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 12; 28pp; English
                                                                                                                                                                                  09-AUG-2001; 2001WO-US041647,
                                                                                                                                                                                                                     09-AUG-2000; 2000US-00635974.
                                                                                                                                                                                                                                                       (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VIWSGGNIDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
ses 15; Conservative
                                                                                                                                                                                                                                                                                                                            WPI; 2002-257423/30.
                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABK11441
                                                                                                           WO200211677-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        he invention
                                                                                                                                              14-FEB-2002
                                                                                                                                                                                                                                                                                            Teufel T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW08939,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                        Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW08939
 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dd
```

```
..
                             Gaps
                             ;
100.0%; Score 88; DB 5; Length 16; 100.0%; Pred. No. 2.9e-07;
                         0; Indels
                         0; Mismatches
```

AAW08939 standard; peptide; 18 AA.

Complementarity determining region 2; CDR2; heavy chain; variable region; reshaped; human; monoclonal; antibody; H225; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate. CDR2 from heavy chain variable region of reshaped H225 antibody.

Homo sapiens

WO9640210-A1

```
The present peptide is the complementarity determining region 2 (CDR2) from the heavy chain variable region of the reshaped human monoclonal antibody (WAb) H225, which is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                        Saldanha JW;
                                                                                                                                                                                                                                                                                                                                 Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 83; 112pp; English.
                                                                                                                                                                                                                             (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                96WO-US009847.
                                                                                                                                95US-00482982.
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 AA;
                                                            1996;
                                                                                                                            07-JUN-1995;
15-DEC-1995;
19-DEC-1996,
```

100.0%; Score 88; DB 2; L 100.0%; Pred. No. 3.3e-07; ive 0; Mismatches 0; 1 VIWSGGNTDYNTPFT 15 2 VIWSGGNTDYNTPFT 16 Local Similarity 100. 16s 15; Conservative Query Match Matches ò

음

·.

Gaps . 0

Length 18; 0; Indels

Heavy chain variable region of 225RD antibody. AAW08953 standard; protein; 119 AA. (first entry) 18-SEP-1997 AAW08953; RESULT 6 AAW08953

Heavy chain; reshaped; monoclonal; antibody; 225RD; human; papidermal growth; temour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDS. Location/Qualifiers Homo sapiens Key Region

50. .65 /label= CDR_2 66. .97 /label= framework_3 .. .30 'label= framework_1 36. .49 __/label= framework_2 /label= CDR_3 109. .119 /label= framework_4 31. .35 /label= CDR_1 . .108 Region Region Region Region Region Region

WO9640210-A1

```
The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RHD. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour calls, especially late stage prostatic tumour calls in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heavy chain; reshaped; monoclonal; antibody; 225RA; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                  - used
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                 Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 88; DB 2; Length 119; 100.0%; Pred. No. 2.7e-06; ive 0; Mismatches 0; Indels
                                                                                                                                    Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heavy chain variable region of 225RA antibody.
                                                                                                                                    Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36. .49
/label= framework_2
50. .65
/label= CDR_2
66. .97
/label= framework_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98. 108
/label= CDR_3
109. 119
/label= framework_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .30
/label= framework_1
31 .35
/label= CDR_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW08950 standard; protein; 119 AA.
                                                                                                                                                                                                                        Claim 30; Fig 22; 112pp; English.
                                                                                                         (MRCC-) MRC COLLABORATIVE CENT
                                                           95US-00482982.
                                   96WO-US009847
                                                                                                (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                            1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 VIWSGGNTDYNTPFT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.
Matches 15: Conservative
                                                                                                                                                             WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                   Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9640210-A1
                                   07-JUN-1996;
                                                           07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW08950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
ö
                                                                                                                                                                                                                The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAb) H225, 225RHA. The MAb is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heavy chain; reshaped; monoclonal; antibody; 225RC; human; epidermal growth factor; BGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                              Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                              Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heavy chain variable region of 225RC antibody.
                                                                                                                     Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36. .49
/label= framework_2
50. .65
/label= CDR_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .30
label= framework_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          framework_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW08952 standard; protein; 119 AA.
                                                                                                                                                                                                Claim 30; Fig 22; 112pp; English.
                                                                                     (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11. .35
/label= CDR_1
                              96WO-US009847.
                                                    95US-00482982.
                                                                                                                                                                                                                                                                                                                                                                                                50 VIWSGGNTDYNTPFT 64
                                                                                                                                                                                                                                                                                                                                                                               1 VIWSGGNIDYNIPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98. .108
/label= CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66. .97
/label= f
                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
es 15; Conservative
                                                                                                                                           WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                               Sequence 119 AA
                                                                                                                      Goldstein NI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                              07-JUN-1996;
                                                    07-JUN-1995;
15-DEC-1995;
          19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW08952
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
ઠે
```

ö

WO9640210-A1

```
The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RHB. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells, especially can prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heavy chain; reshaped; monoclonal; antibody; 225RE; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                          Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                     Length 119;
                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 88; DB 2; Length 11 100.0%; Pred. No. 2.7e-06; Live 0; Mismatches 0; Indels
                                                                                                                                               Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heavy chain variable region of 225RE antibody.
                                                                                                                                           Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .30
/label= framework_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36. .49
/label= framework_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66. .97 /
/label= framework_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109. .119 // label= framework_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW08954
ID AAW08954 standard; protein; 119 AA.
                                                                                                                                                                                                                                Claim 30; Fig 22; 112pp; English.
                                                                                                      (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98. .108
/label= CDR_3
109. .110
                                                                    95US-00482982.
95US-00573289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31. .35
/label= CDR_1
                                            96WO-US009847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50. .65
/label= CDR_2
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                    WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                         Sequence 119 AA;
                                                                                                                                             Goldstein NI,
                                          07-JUN-1996;
                                                                   07-JUN-1995;
15-DEC-1995;
                   19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW08954;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                              The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAb) H225, 225RHC. The MAb is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                   Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour; cell;
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heavy chain; reshaped; monoclonal; antibody; 225RB; human; epidermal growth factor; EGF; receptor; inhibition; growth; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 88; DB 2; Length 119; 100.0%; Pred. No. 2.7e-06; ive 0; Mismatches 0; Indels
                                                                                                                                   Goldstein NI, Giorgio NA, Jones ST, Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heavy chain variable region of 225RB antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31...35

/ label= CDR_1

36...49

/ label= framework_2

50...65

/ label= CDR_2

66...97

/ label= framework_3

98...108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR_3
109. 119
/label= framework_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .30
/label= framework_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW08951 standard; protein; 119 AA.
                                                                                                                                                                                                                         Claim 30; Fig 22; 112pp; English.
                                                                                               (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT
                                                            95US-00482982,
95US-00573289,
                                      96WO-US009847
                                                                                                                                                                                                                                                                                                                                                                                                                            1 VIWSGGNIDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                            50 VIWSGGNTDYNTPFT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                              WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                   Sequence 119 AA;
                                   07-JUN-1996;
                                                            07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW08951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW08951
```

ö

Gaps

. 0

Thu Oct 14 09:36:56 2004

Saldanha JW Giorgio NA, Jones ST, (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT. Goldstein NI,

WPI; 1997-051897/05.

Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.

Claim 30; Fig 22; 112pp; English.

The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RHE. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour calls, especially late stage prostatic tumour calls in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor

Sequence 119 AA;

Gaps ö 100.0%; Score 88; DB 2; Length 119; 100.0%; Pred. No. 2.7e-06; Live 0; Mismatches 0; Indels Local Similarity 100. nes 15; Conservative Query Match Matches

ö

g

AAW08947 standard; protein; 138 AA. AAW08947; RESULT 11

18-SEP-1997 (first entry)

Heavy chain variable region of 225RA antibody.

Heavy chain; reshaped; monoclonal; antibody; 225RA; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region.

Homo sapiens

WO9640210-A1

19-DEC-1996.

95US-00482982 95US-00573289 07-JUN-1995; 15-DEC-1995;

96WO-US009847

07-JUN-1996;

(IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT

Saldanha JW; Goldstein NI, Giorgio NA, Jones ST,

WPI; 1997-051897/05. N-PSDB; AAT49346

Chimeric and humanised versions of anti-EGF receptor antibody 225 - used

ö The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAb) H225, 225RHA. The MAb is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor Gaps for inhibiting tumour growth, esp. of late stage prostatic tumour. ö 100.0%; Score 88; DB 2; Length 138; 100.0%; Pred. No. 3.2e-06; ative 0; Mismatches 0; Indels Claim 31; Fig 20; 112pp; English. 1 VIWSGGNIDYNIPFI 15 69 VIWSGGNIDYNTPFT 83 Query Match Best Local Similarity 100. Matches 15, Conservative Sequence 138 AA; 셤 ઠ

RESULT 12

AAW08944 standard; protein; 138 AA. (first entry) 18-SEP-1997 AAW08944;

Heavy chain variable region of C225 antibody.

Heavy chain; murine; mouse; monoclonal; antibody; C225; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; chimeric.

Mus; spp. Homo sapiens. Synthetic. Chimeric. WO9640210-A1.

19-DEC-1996

96WO-US009847. 07-JUN-1996;

(MRCC-) MRC COLLABORATIVE CENT. 95US-00482982. (IMCL-) IMCLONE SYSTEMS INC 07-JUN-1995; 15-DEC-1995;

Saldanha JW; Boldstein NI, Giorgio NA, Jones ST,

WPI; 1997-051897/05. N-PSDB; AAT49343.

Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour. Example IV; Fig 16; 112pp; English.

- nsed

The present sequence is the heavy chain variable region of the chimeric monoclonal antibody (MAb) C225, which is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to thinbit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras cell cycle inhibitor

Sequence 138 AA;

```
Bivalent fusion proteins that bind epidermal growth factor receptor canalogues – and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                   Single chain antibody; scFv; monoclonal antibody; MAb; EGF; epidermal growth factor; receptor; antitumour; cancer; therapy.
                                                                                                                                                                                                                                                                    1. .119

/label= VH region

/note= "monoclonal antibody 225 VH"

120. .13

/label= Linker

/note= "synthetic spacer peptide"

/label= VL
                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "monoclonal antibody 225 VL"
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                            Single chain antibody scFv(225)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95EP-00106275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmidt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-478748/48.
N-PSDB; AAT42033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 240 AA;
                     29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP739984-A1
                                                                                                                                                             Mus; sp.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wels W,
                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                               Key
Region
                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the heavy chain variable region of the murine monoclonal antibody (MAD) M225, which is specific for the human epidermal growth factor (BGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stages prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                       Heavy chain, murine, mouse, monoclonal, antibody, M225; human, epidermal growth factor; EGF; receptor; inhibition, growth; tumour, cell; late stage; prostatic; prostate; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - used
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
            100.0%; Score 88; DB 2; Length 138; larity 100.0%; Pred. No. 3.2e-06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goldstein NI, Giorgio NA, Jones ST, Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 88; DB 2; L
Pred. No. 3.2e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                Heavy chain variable region of M225 antibody.
                                                                                                                                                                                                                                  AAW08942 standard; protein; 138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example IV; Fig 14; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW05133 standard; protein; 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00482982.
95US-00573289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US009847.
                                                                                              15
                                                                                                                      69 VIWSGGNTDYNTPFT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                          1 VIWSGGNTDYNTPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FINITE TABLE TABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VIWSGGNIDYNTPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-051897/05.
                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT49340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1996;
        Query Match
Best Local Simi]
Matches 15; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-1996.
                                                                                                                                                                                                                                                                                                                    27-AUG-2003
18-SEP-1997
                                                                                                                                                                                                                                                                             AAW08942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW05133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
AAW05133
ID AAW05
XX
AC AAW05
                                                                                                                               d
                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
```

ä

```
ö
                                            scFv(225) (AAW05133) comprises the single-chain binding region of murine monoclonal antibody 225, which is specific for the human epidermal growth factor receptor. It is encoded by plasmid pWW152-225 (see also AAT42033), constructed by cloning MAD 225 wh and VL region cDNAs into plasmid pWW152. Novel bivalent proteins (see also AAW6134-44), some of them including scFv(225) and an effector e.g. cytotoxin, can be produced in bacterial host cells, and are useful as antitumour agents
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                             100.0%; Score 88; DB 2; Length 240; 100.0%; Pred. No. 5.9e-06; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą
Example 2; Page 17; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW05135
ID AAW05135 standard; protein; 65
XX XX
XX DT 29-JAN-1997 (first entry)
XX SCFV(225)-ETA fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                             1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                         50 VIWSGGNTDYNTPFT 64
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserv
```

us-09-635-974a-4.rag

```
scFv(225)-ETA (AAW05135) comprises the single-chain binding region (see also AAW05133) of murine monoclonal antibody 225, which is specific for human epidedrmal growth factor receptor, joined to exotoxin A (ETA). It is encoded by plasmid psw202-225 (see also AAT42035) obtd. by 14gating an scFv(225) gene (AAT42033) into plasmid psw200 contg. the Pseudomonas acruginosa PAK ETA gene. The construct can be used to produce novel bivalent fusion proteins (see also AAW05136-44) in bacterial host cells, for use as antitumour agents
Single chain antibody; scFv; monoclonal antibody; MAb; EGF; epidermal growth factor; receptor; plasmid pSW202-225; cancer; therapy; antitumour; exotoxin A; ETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           72. .38

/label= Spacer

39. .278

/label= scFv(225)

279. .289

/label= Spacer

290. .651

/label= ETA

/note= "exotoxin A amino acids 252-613"
                                                                                                                                                                                                                                                                                                                               . .21
/label= Sig peptide
/note= "ompA signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 19-20; 52pp; English
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schmidt M, Groner B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95EP-00106275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95EP-00106275.
                                                                                                                                              Mus sp.
Pseudomonas; aeruginosa.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-478748/48.
N-PSDB; AAT42035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 651 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP739984-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wels W,
                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                SOURCE COURT AND STATE STATES STATES SOURCE SOURCE
```

ö

Gaps . 0

Search completed: October 6, 2004, 16:29:43 Job time : 76.7895 secs

Š

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

October 6, 2004, 16:23:59 ; Search time 15.7895 Seconds (without alignments) 91.382 Million cell updates/sec Run on:

US-09-635-974A-4 88 Title: Perfect score:

1 VIWSGGNTDYNTPFT 15 Sequence:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SI	Description	Iq heavy chain V	heavy cha	heavy chain pr	heavy chain	heavy	heavy	mu chain pre	-DNA aut	eavy	eavy	amma -	amma-1 chain	eavy chain V	aw	eavy	awy		ď	2 dehydroge	Δ.	heavy chain	g heavy chain V	Ig heavy chain V r	g heavy chain V	g heavy chai	g heavy c	g heavy chai	g heavy cha	y 1 mission of
SUMMARIES	Ü	PH1026	\sim	1	7	2	rΛ	33	5	9	8	91	23	32	8	2	2	838563	5	35	42	0	9	2	8	σ,	S14493	Ö	0	0
	DB	N	~	~	~	7	Н	N	N	N	N	~	7	7	~1	~	~	~	7	7	~	7	N	~	Ċ	N	~	Ŋ	~	N
	Length	109	96	0	\rightarrow			\rightarrow	Н	N	$^{\circ}$	m	4	н	0	N	4	117	m	m	IO	σ,	0	0	O	0	107	0	0	н
J	Query Match	76.1		ω.	ω.	w.	73.9	ω.	щ.	۳.	m	m	e,	'n.	œ,	œ.	œ	67.0	'n.	ä	ä	ö	ö	ö	ö	ö	。	ö	ö	ö
	Score	9	65	65	65	65	65	65	65	65	65	65	65	64	09	9	09	59	28	54	54	53	53	53	53	23	23	53	23	23
	Result No.		7	n	4	ស	9	7	α	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58

heavy chain	heavy	chain	Ig heavy chain V r	arginase - Deinoco	Ig heavy chain V r	Ig heavy chain V r									
S11100	S11108	S11101	S11099	S11104	S11106	S11105	S11103	S11102	S10111	PL0087	A49049	S52446	H75493	S14491	PH1024
0	N	N	0	N	N	0	N	7	N	N	N	(1)	N	N	N
112	112	113	114	114	114	114	115	116	117	120	122	141	301	107	110
-															
60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	60.2	59.1	59.1
	e	۳	m	m	m	m	53 60.2	m	m	e	m	53 60.2	е	N	2

RESULT 1

Ig heavy chain V region (clone 163-c3) - mouse (fragg C; Species: Mus musculus (house mouse) C; Species: 30-89-1933 #sequence_revision 30-Sep-1993 ## C; Accession: PH1026 R; Tillman, D.M.; JOU, N.T.; Hill, R.J.; Marion, T.N. J. Exp. Med. 176, 761-779, 1992 A; Title Both IgM and IgG anti-DNA antibodies are the A; Reference number: PH0971; MUID:92381444; PMID:1512; A; Residues: nucleic acid sequence not shown A; Molecule type: mRNA A; Residues: 1-109 cTIL- A; Experimental source: B cell, strain [NZB x NZM]FI C; Superfamily: immunoglobulin V region; immunoglobulic; Keywords: heterotetramer; immunoglobulin C; Keywords: heterotetramer; immunoglobulin F; IS-97/Domain: immunoglobulin homology <inm> Query Match Best Local Similarity 78.6%; Pred. No. 0.0018; Matches II; Conservative I; Mismatches 2,</inm>	3CU 1HG	
C;Species: Mus musculus (house mou C;) Date: 30-Sep-1993 #sequence_revi C;Accession: PH1026 R;Tillman, D.M.; Jou, N.T.; Hill, J. Exp. Maci. 176, 761-779, 1992 A;Tille: Both IgM and IgG anti-DMA A;Reference number: PH0971; MUID: 9 A;Accession: PH1026 A;Accession: PH1026 A;Status: nucleic acid sequence no A;Molecule type: mRNA A;Residues: 1-109 < TILL. A;Experimental source: B cell, str C;Superfamily: immunoglobulin V re C;Superfamily: immunoglobulin V re C;Superfamily: immunoglobulin hom Query Match Query Match Query Match Matches II; Conservative I	Iq heavy chain V region (clone 163-c3) - mouse (fragment)	
C;Date: 30-Sep-1993 #sequence_revi C;Accession: PH1026 R;Tillman, D.M.; Jou, N.T.; Hill, J. Exp. Med. 176, 761-779, 1992 A;Tille: Both IgM and IgG anti-DNA A;Reference number: PH0971; MUID:9 A;Accession: PH1026 A;Status: nucleic acid sequence no A;Molecule type: mRNA A;Residues: 1-109 <til-> A;Experimental source: B cell, str C;Superfamily: immunoglobulin V re C;Keywords: heterotetramer; immuno F;IS-97/Domain: immunoglobulin hom Query Match Query Match Conservative 1</til->	C; Species: Mus musculus (house mouse)	
C,Accession: PH1026 R;Tilman, D.M.; Jou, N.T.; Hill, J, Exp. Med. 176, 761-779, 1992 A;Title: Both 1gM and 1gG anti-DNA A,Reference number: PH0971; MUID: 9 A;Accession: PH1026 A;Status: nucleic acid sequence no A;Molacule type: mRNA A;Residues: 1-109 cfIL-> A;Experimental source: B cell, str C;Superfamily: immunoglobulin V re C;Keywords: heterotetramer; immunoglobulin hom C;Keywords: heterotetramer; immunoglobulin hom C;Keywords: immunoglobulin hom Cuery Match Best Local Similarity 78:6%; Matches 11; Conservative 1	C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996	hange 16-Aug-1996
R; Tillman, D.M.; Jou, N.T.; Hill, U. Exp. Med. 176, 761-779, 1992 A; Title: Both IgM and IgG anti-DNB A; Reference number: PH0971; MUID:9 A; Accession: PH1026 A; Accession: PH1026 A; Molecule type: mRNA A; Molecule type: mRNA A; Mesidues: 1-109 < TILL A; Experimental source: B cell, str C; Superfamily: immunoglobulin V re C; Keywords: heteroteramer; immunog; Keywords: heteroterteramer; immunog; Keywords: heteroteramer; immunoglobulin hom Quuery Match Matches 11; Conservative 1	C;Accession: PH1026	
J. Exp. Med. 176, 761-779, 1992 A.Title: Both Igm and IgG anti-DNA A;Reference number: PH0971; MUID:9 A;Accession: PH1026 A;Status: nucleic acid sequence no A;Molecule type: mRNA A;Residues: 1-109 <tild 11;="" 1<="" a;experimental="" b="" c;keywords:="" c;superfamily:="" cell,="" conservative="" domain:="" f;15-97="" heterotetramer;="" hom="" immuno="" immunoglobulin="" match="" matches="" n="" query="" re="" source:="" str="" th="" v=""><th>R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.</th><th></th></tild>	R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.	
A;Title: Both IgM and IgG anti-DNA A;Reference number: PH0971; MUID: 9 A;Accession: PH1026 A;Status: nucleic acid sequence no A;Molecule type: mRNA A;Residues: 1-109 <til> A;Experimental source: B cell, str C;Superfamily: immunoglobulin V re C;Superfamily: immunoglobulin V re C;Keywords: heterotetramer; immunoglobulin hom Query Match Query Match Query Match Query Match A; Best Local Similarity 78:6%; Matches 11; Conservative 1</til>	J. Exp. Med. 176, 761-779, 1992	
A; Reference number: PH0971; MUID:9 A; Accession: PH1026 A; Status: nucleic acid sequence no A; Molecule type: mRNA A; Residues: 1-109 < TIL. A; Experimental source: B cell, str C; Superfamily: immunoglobulin V re C; Keywords: heteroterramer; immuno F; 15-97/Domain: immunoglobulin hom Query Match Best Local Similarity 78.65; Matches 11; Conservative 1	A; Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective	ucts of clonally sel
A;Accession: PH1026 A;Status: nucleic acid sequence no A;Molecule type: mRnA A;Residues: 1-109 <til> A;Experimental source: B cell, str C;Superfamaily: immunoglobulin V re C;Superfamaily: immunoglobulin V re C;Keywords: hererotetramer; immunoglobulin hom P;15-97/Domain: immunoglobulin hom Query Match Best Local Similarity 78.6%; Matches 11; Conservative 1</til>	A; Reference number: PH0971; MUID:92381444; PMID:1512540	•
A;Status: nucleic acid sequence no A;Molecule type: mRNA A;Residues: 1-109 <tll>A;Experimental source: B cell, str C;Superfamily: immunoglobulin V re C;Keywords: heterotetramer; immunoglobulin hom Query Match Query Match Query Match Matches 11; Conservative 1</tll>	A; Accession: PH1026	
A;Molecule type: mRNA A;Residues: 1-109 <tii.> A;Residues: 1-109 <tii.> A;Experimental source: B cell, str C;Superfamily: immunoglobulin V re C;Keywords: heteroterramer; immuno F;15-97/Domain: immunoglobulin hom Query Match Best Local Similarity 78.6%; Matches 11; Conservative ;</tii.></tii.>	A.Status: nucleic acid sequence not shown	
A;Residues: 1-109 <til> A;Experimental source: B cell, str C;Superfamily: immunoglobulin V re C;Keywords: heterotetramer; immunoglobulin hom F;15-97/Domain: immunoglobulin hom Query Match Best Local Similarity 78.6%; Matches 11; Conservative 1</til>	A; Molecule type: mRNA	
A; Experimental source: B cell, str C; Superfamily: immunoglobulin V re C; Keywords: heterotetramer; immunog F;15-97/Domain: immunoglobulin hom Query Match Deet Local Similarity 78.6%; Matches 11; Conservative 1	A;Residues: 1-109 <til></til>	
C;Superfamily: immunoglobulin V re C;Keywords: heteroterramer; immuno F;15-97/Domain: immunoglobulin hom Query Match Best Local Similarity 78.6%; Matches 11; Conservative ;	A; Experimental source: B cell, strain [NZB x NZW] F1	
C;Keywords: heterotetramer; immuno F;15-97/Domain: immunoglobulin hom Query Match Best Local Similarity 78.6%; Matches 11; Conservative 1	C; Superfamily: immunoqlobulin V region; immunoqlobulin homology	ology
F;15-97/Domain: immunoglobulin hom Query Match Best Local Similarity 78.6%; Matches 11; Conservative 1	C: Keywords: heterotetramer: immunoglobulin	
Query Match 76.1%; Best Local Similarity 78.6%; Matches 11; Conservative 1	F,15-97/Domain: immunoglobulin homology <imm></imm>	
Best bocal Similarity 78.58; Matches 11; Conservative 1	Query Match 76.1%; Score 67; DB 2; Length 109;	109;
	Best Local Similarity 78.5%; Fred. NO. U.0018; Matches 11; Conservative 1; Mismatches 2; Indels	els 0; Gaps 0;

ve B

1 VIWSGGNTDYNTPF 14 20 ò d

Agyotz, dain V region (anti-DNA) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A49042
R;Taki, S.; Hirose, S.; Kinoshita, K.; Nishimura, H.; Shimamura, T.; Hamuro, J.; Shirai, Bur. J. Immunol. 22, 987-992, 1992
A;Title: Somatically mutated IgG anti-DNA antibody clonally related to germ-line encodec A;Accession: A49042; MUD:92201320; PMID:1551410
A;Reference number: A49042; MUD:92201320; PMID:1551410
A;Reference number: BNA
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-90 cTAK>
A;Coss.references: GB:S92270; NID:9247954; PIDN:AAB21904.1; PID:9247955
A;Coss.references: GB:S92270; NID:9247954; PIDN:AAB21904.1; PID:9247955
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology cINM>

Gaps . 0 Query Match 73.9%; Score 65; DB 2; Length 90; Best Local Similarity 78.6%; Pred. No. 0.003; Matches 11; Conservative 1; Mismatches 2; Indels

0;

ઠ g

```
Ig heavy chain precursor V region (MC101) - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Species: 14-Nov-1983 #text_change 22-Jun-1999 (Spacession: A02096 # Niyata, T.; Moriwaki, K.; Honjo, T. & Mikaido, T.; Miyata, T.; Moriwaki, K.; Honjo, T. & Mariada, T.; Miyata, T.; Moriwaki, K.; Honjo, T. & Mariada, T.; Miyata, T.; Moriwaki, K.; Honjo, T. & Mariada, T.; Moriada, T.; Moriada, T.; Moriada, T.; Moriada, M.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A33932
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R;Daccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Broc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-li A;Reference number: A33932, MUID:89282823; PMID:2499887
A;Accession: A33932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                         ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig mu chain precursor V region (D23) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 23-May-1997
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;F1-19/Domain: signal sequence #stetus predicted <SIG>
F;10-116/Product: Ig heavy chain V region (MC101) #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>
                                                                                                                                         ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-116 <BAC.
A; Cross-references: GB:M27107
A; Note: the authors translated the codon CTA for residue 18 as C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin N region; immunoglobulin homology
F; 34-116/Donain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.9%; Score 65; DB 2; Length 116; 78.6%; Pred. No. 0.0039; 2; Indels ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 1; Length 116;
Pred. No. 0.0039;
1; Mismatches 2; Indels
                                                                    Length 115
                                                         Score 65; DB 2; Le
Pred. No. 0.0038;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.9%; Scor. 78.6%; Pred. No. v...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
F,15-97/Domain: immunoglobulin homology <IMM>
                                                                    73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 VIWSGGSTDYNAAF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 VIWSGGSTDYNAAF 82
                                                                                                                                                                                                                  1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VIWSGGNIDYNTPF 14
                                                                                                                                                                                                                                                                                       50 VIWSGGSTDYNAAF 63
                                                                 Query Match
Best Local Similarity 78.6'
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 78.6
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 16/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A33932
                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
511107
19 heavy chain V region (clone NQ2-45.10.4) - mouse (fragment)
c; species: Mus musculus (house mouse)
c; Species: Mus musculus (house mouse)
c; Accession: Sll107
R; Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A; Pitle: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A; Pitle: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A; Accession: Sll107
A; Reference number: S07331; MUD:83271467; PMID:6877353
A; Accession: Sll107
A; Status: preliminary
A; Residues: mRNA
A; Residues: 1-115 < kAA>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                              A25913

A25913

Greavy chain precursor V region (BFL2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 21-Jan-2000

C;Dates: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 21-Jan-2000

C;Dates: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 21-Jan-2000

R;Lawler, Am; Lin, P.S.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987

A;Title: Adult # B-cell repertoire is biased toward two heavy-chain variable-region genes

A;Accession: A25913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
S26470
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26470
R;Kavaler, J.
Submitted to the BMBL Data Library, April 1991
A;Reference number: S26459
A;Reference number: S26470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X59109; NID:g51948; PIDN:CAA41835.1; PID:g51949 C.Superfamally: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-100 <LAW>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keyworfs: heteretramer; immunoglobulin
F,19-100/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; DB 2; Lengtn Luv
Pred. No. 0.0033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.9%; Score 65; DB 2; 78.6%; Pred. No. 0.0038; iive 1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.9%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VIWSGGNIDYNIPF 14
                                                 43 VIWSGGSTDYNAAF 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 VIWSGGSTDYNAAF 63
       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 VIWSGGSTDYNAAF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 78.6
Matches 11, Conservative
       VIWSGGNTDYNTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <KAV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
```

g

ð g ·.

Gaps

. 0

```
Ig gamma-1 chain precursor (15C5) - mouse (fragment)
Cispecies: Mus musculus (house mouse)
Cispecies: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
CiAccession: 514238
Extractions A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D. Bur. J. Biochem. 192, 767-775, 1990
A;Title: Construction and characterization of a recombinant murine monoclonal antibody dateference number: $14236; MUID:91006173; PMID:2209622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S31913

*R; Bespalov, I.A.; Hiyanov, P.A.; Lukashevich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponov submitted to the EMBL Data Library, January 1993
A; Reference number: S31913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-140 «VAN»
A; Residues: 1-140 «VAN»
A; Cross-references: EMBL:X6392; NID:g51619; PIDN:CAA39803.1; PID:g747853
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
P; 26-108/ Domain: immunoglobulin homology «IMM»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Accession: 331933
A/Molecule type: mRNA
A/Residues: 1-135 <- RES.
A/Cross-references: EMBL:X70822; NID:g57921; PIDN:CAA50153.1; PID:g57922
A/Experimental source: strain BALB/c
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; Reywords: heterotetramer; immunoglobulin predicted <SIG>F; 1-11/Domain: signal sequence #status predicted <SIG>F; 1-115/Product: Ig gamma-2A chain (fragment) #status predicted <MAT>F; 34-116/Domain: immunoglobulin homology <IPM>
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 140;
                                                                                       73.9%; Score 65; DB 2; Length 127
78.6%; Pred. No. 0.0043; Lindels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65; DB 2; Length 135
Pred. No. 0.0046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.9%; Score 65; DB 2; Length 140
78.6%; Pred. No. 0.0047;
.ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S26321
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig. gamma-2A chain precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.9%;
                                                                                                                                                                                                                                       1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VIWSGGNIDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 VIWSGGSTDYNAAF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VIWSGGSTDYNAAF 74
                                                                                                 Query Match
Best Local Similarity 78.6'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                             50 VIWSGGSTDYNAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VIWSGGNTDYNTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S14238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $14238
                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                             요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p30560

130560

130 heavy chain V region (36.1.2D) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change 23-Jul-1999

C;Accession: D30560

R;Matcassion: D30560

R;Matcassion: D42, 863-870, 1989

J:Immunol. 142, 863-870, 1989

A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (PACI) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 23-May-1997
C;Accession: B31807
R;Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatth A;Taub, R.; Gould, R.J.; Hassion: B31807
A;Title: A monoclonal antibody against the platelet fibrinogen receptor contains a seque A;Reference number: A31807; MUID:89079661; PMID:2909518
A;Accession: B31807
A;Accession: preliminary
A;Accession: preliminary
A;Reterence mRNA
A;Residues: 1-127 cTAU>
                                                                                                             C,Accession: PL0198
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Fite: Variable region primary structures of monoclonal anti-DNA autoantibodies from A;Feterace number: PL0198; MUID:90309768; PMID:2114528
A;Accession: PL0198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                     anti-DNA autoantibody BV16-13, heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A/Accession: D30560
A/Status: preliminary
A/Status: mRNA
A/Accoule type: mRNA
A/ACross-references: GB:MZ4271; NID:g195617; PIDN:AAA38372.1; PID:g195618
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                   A/Molecule type: mRNA
A,Residues: 1-116 <SMI>
A,Residues: 1-116 <SMI>
A,Cross-references: GB(NES1638; NID:g50191; PIDN:CAA37689.1; PID:g930137
C,Superfamily: immunoglobulin V region; immunoglobulin homology
F,15-97/Domain: immunoglobulin homology <IMM>
F,15-97/Domain: immunoglobulin homology <IMM>
F,15-97/Region: complementarity-determining 1
F,50-65/Region: complementarity-determining 2
F,95-105/Region: complementarity-determining 3
F,95-101/Region: D_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.9%; Score 65; DB 2; Length 121; Best Local Similarity 78.6%; Pred. No. 0.0041; Matches 11; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65; DB 2; Length 116
Pred. No. 0.0039;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A30560; MUID:89110062; PMID:2464028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.9%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 'o...
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 VIWSDGRIDYNVPF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIWRGGNTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIWSGGNTDYNTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;102-113/Region: JH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
```

à 셤 ö

Gaps

ô

ö

Gaps

.. 0

ઠે

```
g
                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
33131
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 "#text_change 23-Mar-2001
C;Accession: 83131
C;Accession: 83131
A;Pescription: A humanized anti-tumor necrosis factor alpha monoclonal antibody that act
C,Accession: S14506
R;Chen, Q.; Stenzel-Pocre, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH
A;Reference number: S14484
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Residues: 1-121 < TEM>
A, Residues: 1-121 < TEM>
A, Cross-references: EMBL: 222669; NID: 9297471; PIDN: CAA80378.1; PID: 9297472
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: hererotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Rosidues: 1-107 <CHE>
A;Cross-references: EMBL:X58651; NID:g51291; PIDN:CAA41508.1; PID:g51292
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 121;
                                                                                                                                                                                                                                                                                    Length 114;
                                                                                                                                                                                                                                                                                  Score 64; DB 2; Length 114 Pred. No. 0.0055; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60; DB 2;
Pred. No. 0.022;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 68.2%; Score 60; DB 2; Best Local Similarity 71.4%; Pred. No. 0.025; Matches 10; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                  72.7%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.2%;
ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                 1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                         46 VIWSGGTTDYNAAF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 VIWRGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 78.6'
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S33131
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S14506
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
S14506
                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

Search completed: October 6, 2004, 16:34:46 Job time : 16.7895 secs

neisseria m neisseria m chlorella v streptococc

P43663 P31746 P53935 O862x5 O9fia2 O9jiuv9 O01511 O01511 O02008 P13504

LPPD_SALITY
CDGT_BACS2
YNU1_EAGS2
COAD_WIGHS
TT2_ĀRĀTH
YR2_ĀRĀTH
WR14_NETMB
WRC1_CHVM1
MTC1_CHVM1
AROB_STRREN

359 1240 1240 168 168 259 259 259 355 364 576

photobacter mus musculu

ALIGNMENTS

bacillus sp saccharomyc wiggleswort arabidopsis

salmonella

```
RESULT 1
HV45 MOUSE
                                                                                                                                                                                                                                                       mus musculu
trichophyto
podospora a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 emericella
                                                                          October 6, 2004, 16:21:13 ; Search time 9.21053 Seconds (without alignments) 84.800 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P511628
P5533018
P5533018
P561176
P561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P01821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P20679
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                        141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
TRIRU
PODAN
EMENI
YEAST
HUMAN
MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
MOUSE
NEUCR
DROME
MOUSE
                                                     protein search, using sw model
                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HV44
HV43
HV5M
NU5M
PIG1
                                                                                                                                                                  1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                 US-09-635-974A-4
88
                                                                                                                                                                                                                                                                                                                                                                                               SwissProt_42:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                        ı
                                                       OM protein
                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                        Searched:
                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
No.
```

HV45 MOUSE STANDARD; PRT; 116 AA.
P01821;
P01821;
21-JUL-1986 (Rel. 01, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 g heavy chain V region MC101 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

xenopus lae xenopus lae xenopus lae rana catesb homo sapien bacillus oh

XENLA XENLA XENLA RANCA

HUMAN BACOH BIFLO

NEUCR BOVIN RHIST SHEEP

XENLA

CDGT HIS4 ARGI ARG2

mus musculu rattus norv

neurospora drosophila

bos taurus rhizopus st ovis aries

P22300 P50367 097704

sapien mus musculu sarcophaga drosophila homo sapien homo sapien

homo

Q96qk1

HUMAN MOUSE SARPE

AT10 HUMAN MANR_HUMAN

440 1077 1456

DROME

neurospora homo sapien

xenopus lae

RESULT 2 NUSM_TRIRU

```
Q01561; Q9T9N1;
01-UUN-1994 (Rel. 29, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991 (Rel. 17, Created)
1-FEB-1991 (Rel. 17, Last sequence update)
01-UTL-1993 (Rel. 26, Last annotation updaté)
NADH-ubdiquinone oxidoreductase chain S (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y18476; CAA77185.1; -.
EMBL; X65223; CAA46329.1; -.
PIR, S26950; S26950.
InterPro; IPR003916; NADHub_oxred5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001750; Oxidored q1.
InterPro; IPR001516; Oxidored q1.
Pfam, PF00361; oxidored q1, 1.
Pfam; PF00662; oxidored q1, 1.
PRINTS; PR01434; NADHDHGNASES.
                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=IP 1817.89;
MEDLINE=99146870; PubMed=10022946;
                                                                                                                                                                                                                       [2]
SEQUENCE OF 1-337 FROM N.A.
STRAIN=IP 1817.89;
MEDLINE=92405249; PubMed=1326416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 IİWSFGNLDYSTVFS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 60.0
Matches 9; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                    Trichophyton rubrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Podospora anserina.
                                                                                                                     NCBI_TaxID=5551;
                                                                               Mitochondrion.
                                                         OR NADHS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUSM PODAN
ID NUSM PODAN
AC P20679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its must by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cummings D.J., McNally K.L., Domenico J.M., Matsuura B.T.; "The complete DNA sequence of the mitochondrial genome of Podospora
                                                                                                                                                                                        STRAIN=s, and A; which was a strain and A; which we will a strain 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=YA2 / PYROA4 / CXXC3;
MEDLINE=89296483; PubMed=2662141;
Brown T.A., Constable A., Ray J.A., Waring R.B., Scazzocchio C., Davies R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Curr. Genet. 17:375-402(1990).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                     Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Emericella nidulans (Aspergillus nidulans).
Mitoohondripu.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.0%; Score 51; DB 1; Length 652; 53.3%; Pred. No. 2.1; ive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase, NAD, Ubiquinone, Mitochondrion.
SEOUENCE 652 AA: 72632 MW; 84CA887B75755FE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUSM EMENI STANDARD; PRT; 657 AA.
P11628; Q00181;
P10-0CT-1998 (Rel. 12, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, X55026; CAA38798.1; -.
PTR, 509133; S09133.
InterPro; IPR003918; NADHub_oxred4.
InterPro; IPR001916; NADHub_oxred5.
InterPro; IPR00176; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1.
Pfam; PF00361; oxidored_q1.
PRINTS; PR01434; NADHDHGNASE5.
PRINTS; PR01434; NADHDHGNASE5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90291512; PubMed=2357736;
                                                                                                                                                                                                                                                                                                                                                           J. Mol. Biol. 212:269-286(1990)
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 ILWSLGNLDYSTVFS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 53.3
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  652 AA;
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLETE GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cummings D.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anserina."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUSM_EMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its must by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        de Bievre C., Dujon B.;
"Mitochondrial DNA sequence analysis of the cytochrome oxidase
"Mitochondrial DNA sequence analysis of the cytochrome oxidase
subunit I and II genes, the ArPase9 gene, the NADH dehydrogenase ND4L
and ND5 gene complex, and the glutaminy1, methiony1 and arginy1 tRNA
genes from Trichophyton rubrum.";
curr. Genet. 22:229-234(1992).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     de Bievre C., Dujon B.;
"Organisation of the mitochondrial genome of Trichophyton rubrum III.
DNA sequence analysis of the NADH dehydrogenase subunits 1, 2, 3, 4,
5 and the cytochrome b gene.";
Curr. Genet. 35:30-35(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                        Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.4%; Score 54; DB 1; Length 653; 60.0%; Pred. No. 0.7; 3; Indels cive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase, NAD, Ubiquinone, Mitochondrion.
SEQUENCE 653 AA, 73456 MW, 58207B990F568E14 CRC64;
653 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  652 AA
```

ö

Gaps

.. 0

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arginase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARGI HU
P05089;
                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
          NO REPORT OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
"Nucleotide sequence of the Aspergillus nidulans mitochondrial gene for subunit 5 of NADH dehydrogenase."; Nucleic Acids Res. 17:4371-4371(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "DNA sequence analysis of a 23,002 bp DNA fragment of the right arm of Saccharomyces cerevisiae chromosome VII.";
Yeast 13.357-163(1997).
-- SIMILARITY: SOME, TO YEAST UTR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=S288C;
MEDILINE=97279231; PubMed=9133739;
Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez-Perez M.,
Nombela C.;
                                                                                                                        SEQUENCE OF 316-349 FROM N.A.
STRAIN=NRRL 322;
STRAIN N.G., Wientjes F.J.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycoties; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 52.8 kDa protein in BUBI-HIP1 intergenic region.
YGR189C OR G7553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.0%; Score 51; DB 1; Length 657; 57.1%; Pred. No. 2.1; 3; Indels ive 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BSBB679A151E7287 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, X15011; CAA33116.1; --
EMBL; X6299; CAA4727.1; --
EMBL; S04724; S04727.1; --
EMBL; S04724; S04727.1; --
EMBL; S04724; S04727.1; --
InterPro; IPR0013916; NADHub oxred5.
InterPro; IPR00155; Oxidored q1.
Ffam; PF00361; Oxidored q1; 1.
FRINTS; PR01434; NADHDHGNASES.
Oxidoreductase; NADHDHGNASES.
OXIGORGUCESES, OXIGORGUS SERVINS; RICCHONDITION, SEQUENCE 657 AA; 73361 MW; B5BB679A151E7287 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z72974; CAA97215.1; -. EMBL; X99074; CAA67525.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 ILWSFGNIDYSTVF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 57.1 tes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YG46 YEAST
P53301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YG46_YEAST
   SA W D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R D R D R D R D R D R D R D R D R D R D R D R D R D D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
TISSUE=Liver;

MEDLINE=22380257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Ditchenco L., Marusina K., Farmer A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takiguchi M., Haraguchi Y., Mori M.;
"Human liver-type arginase gene: structure of the gene and analysis
of the promoter region.";
Nucleic Acids Res. 16:8789-8802(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and nucleotide sequence of cDNA for human liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٦,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haraguchi Y., Takiguchi M., Amaya Y., Kawamoto S., Matsuda I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50.5; DB 1; Length 507;
Pred. No. 1.9;
2; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracey A.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                POLY-SER.
7D7B61F57AEA942C CRC64;
PIR; S64507; S64507.
HSSP; P23904; LAUK.
Germonine; 141501; -.
SGD; S0003421; CRH1.
GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
GO; GO:0000131; C:incipient bud site; IDA.
InterPro; IPR000955; Conalike lec gl.
InterPro; IPR000757; Glycohydrolf.
Pfam; PF00722; Glycohydrolf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arginase.";
Proc. Natl. Acad. Sci. U.S.A. 84:412-415(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1987 (Rel. 05, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Arginase 1 (EC 3.5.3.1) (Liver-type arginase)
                                                                                                                                                                                                                                                                                                               POLY-SER.
POLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87092419; PubMed=3540966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89016562; PubMed=3174433;
                                                                                                                                                                                                                                                                                                            301 310 POO
345 357 POO
387 391 POO
467 470 POO
507 AA; 52757 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.4%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 WAGGETNYNDAPFT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 WSGGNTDYN-TPFT 15
```

.. ;;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Farteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Youdhan A., Rodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.S., Schmutz J., Myers R.M., Schwinski M.I., Skhalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uchino T., Haraguchi Y., Aparicio J.M., Mizutani N., Higashikawa M., Naitoh H., Mori M., Matsuda I.; There over a mutations in the liver-type arginase gene in three unrelated Japanese patients with argininemia."; Am. J. Hum. Genet. 51:1406-1412(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS ARGININEMIA THR-11 AND VAL-138.
MEDLINE=9537725; PubMed=7649538;
Wichino T., Snyderman S.E., Lambert M., Qureshi I.A., Shapira S.K., Sansaziog C., Smit L.M.E., Jakobs C., Mateuda I.;
"Molecular basis of phenotypic variation in patients with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT SER-290.
MEDLINE=92286280; PubMed=1598908;
Grody W.W., Klein D., Dodson A.E., Kern R.M., Wissmann P.B.,
Goodman B.K., Bassand P., Marescau B., Kang S.-S., Leonard J.V.,
Cederbaum S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular genetic study of human arginase deficiency."; Am. J. Hum. Genet. 50:1281-1290(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 207800; -.
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0004053; F:arginase activity; TAS.
GO; GO:0006527; P:arginine catabolism; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M14502; AAA51776; 1; ---
EMBL; X12662; CAA31188.1; ---
EMBL; X12663; CAA31188.1; JOINED.
EMBL; X12664; CAA31188.1; JOINED.
EMBL; X12665; CAA31188.1; JOINED.
EMBL; X12666; CAA31188.1; JOINED.
EMBL; X12666; CAA31188.1; JOINED.
EMBL; X12669; AAE370.
EMBC; X12669; AAE370.
EMBC; X12669; AAE370.
EMBC; X12669; AAE370.
EMBC; X126699; AAE370.
EMBC; X126699; AAE370.
                                                                                                                                                                                                                                                                                                                                                           VARIANT ARGININEMIA ARG-235.
MEDLINE=93098256; PubMed=1463019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            argininemia.";
```

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=22389257; PubMed=1247932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

R. Klausner R.D., Tordan H., Moore T., Mans S.I., Wang J., Hsieh F.,

A plachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B. Diacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong D.,

R. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B. Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

R. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Villalon D.K., Moterman M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                    MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
I (in argininemia; 12% of wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_015594.

G -> V (in argininemia).

FTId=VAR_01559.

G -> R (in argininemia).

/FTId=VAR_000674.

/FTId=VAR_000675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.8%; Score 50; DB 1; Length 322; 60.0%; Pred. No. 1.4;
InterPro; IPR006035; Arg agm_form.

Refam; PR00491; arginase.

Refam; PR00416; ARGINASE.

RENINTS; PR00116; ARGINASE.

RESOSITE; PS00147; ARGINASE.

RESOSITE; PS01043; ARGINASE.

RESOSITE; PS01053; ARGINASE.

RESOSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chieko H.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> Q (IN REF. 1).
8F3BE2652243F622 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Arginase 1 (EC 3.5.3.1) (Liver-type arginase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6 X CBA; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34735 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 VIWVDAHTDINTPLT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 60.0 es 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARGI MOUSE
Q61176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                          METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARGI_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                       ò
```

ö

D.W.;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                               MEDLINE=87194847; PubMed=3571256; Kawando S., Amaya Y., Murakani K., Tokunaga F., Iwanaga S., Kobayashi K., Saheki T., Kimura S., Mori M.; "Complete nucleotide sequence of cDNA and deduced amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).

X O'D., Kim N.N., Traish A.M., Christianson D.W.;

A Cox J.D., Kim N.N., Traish A.M., Christianson D.W.;

A cox J.D., Kim N.N., Traish A.M., Christianson D.W.;

T erectile function...;

IN Nat. Struct. Biol. 6:1043-1047(1999).

I. Nat. Struct. Biol. 6:1043-1047(1999).

- CATALYTIC ACTIVITY: L-arginine + H(2)0 = L-ornithine + urea.

- CATALYTIC ACTIVITY: L-arginine + H(2)0 = L-ornithine + urea.

- SUBUNIT: Homographes.

- SUBUNIT: Homographes.

- SUBUNIT: BOCATION: Cytoplasmic.

- SUBULILLAR LOCATION: Cytoplasmic.

- INDUCTION: By arginine or homographine.

- SIMILARITY: Belongs to the arginase family.
                                                                                                                                                                                                                                                                                         MEDLINE=97002331; PubMed=8849731; Ash D.B., Christianson D.W.; Ash D.B., Christianson D.W.; Structure of a unique binuclear manganese cluster in arginase."; Nature 383:554-557(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97410344; PubMed=9265637; Scolnick L.R., Kanyo Z.F., Cavalli R.C., Ash D.E., Christianson D "Altering the binuclear manganese cluster of arginase diminishes thermostability and catalytic function.", Biochemistry 36:10558-10565(1997).
                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00116; ARGINASE.
TIGRFAMS; TIGR01229; rocF arginase; 1.
PROSITE; PS00147; ARGINASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; MI7931; AAA40760.1; --
EMBL; MI7924; AAA40760.1; --
EMBL; MI7925; AAA40760.1; JOINED.
EMBL; MI7926; AAA40760.1; JOINED.
EMBL; MI7929; AAA40760.1; JOINED.
EMBL; MI7929; AAA40760.1; JOINED.
EMBL; MI7929; AAA40760.1; JOINED.
EMBL; MI7929; AAA40760.1; JOINED.
EMBL; MI7930; AAA40760.1; JOINED.
EMBL; MI7930; AAA40760.1; JOINED.
EMBL; MI7930; AAA40761.1; --
EMBL; MI7930; AAA40761.1; --
EMBL; MI7930; AAA40761.1; --
EMBL; MIRA; 13-MAY-98.
EMBL; SRLA; 13-MAY-98.
EMBL; SRLA; 13-MAY-98.
EMBL; GARA; GARA-01.
EMBL; GARA; GARA-01.
EMBL; GARA; GARA-01.
EMBL; GARA-04-EMBR-01.
EMBL; GARA-04-EMBR-01.
EMBL; GARA-04-EMBR-01.
EMBL; GARA-04-EMBR-01.
                                                                                                                                                                                                 rat liver arginase.";
Biol. Chem. 262:6280-6283(1987)
       Chem. 263:2245-2249(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; IRLA; 15-007-02.
PDB; ZRLA; 13-WAY-98.
PDB; 2RLA; 13-WAY-98.
PDB; 3RLA; 13-WAY-98.
PDB; 5RLA; 13-WAY-98.
PDB; 1HQ5; 04-APR-01.
PDB; 1HQ5; 04-APR-01.
PDB; 1HQ5; 04-APR-01.
PDB; 1HQ7; 04-APR-01.
PDB; 1HQ7; 04-APR-01.
PDB; 1HQX; 31-DBC-02.
InterPro; IPR006035; Arginase.
InterPro; IPR006035; Arginase.
PERM; PF00491; arginase.
                                                    FROM N.A.
                                                       SEQUENCE
          Biol.
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUB-Liver;
MEDLINE-8811534; PubMed=2892837;
Ohtake A., Takiguchi M., Shigeto Y., Amaya Y., Kawamoto S., Mori M.;
"Structural organization of the gene for rat liver-type arginase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Indeneration and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."; of more than 15,000 full-length
broc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-ornithine + urea.
-!- COFACTOR: Manganese.
-!- PATHWAY: Arginine degradation via the urea cycle; first step.
-!- SUBUCELLULAR LOCATION: Cycoplasmic.
-!- SUBCELLULAR LOCATION: Cycoplasmic.
-!- SIMILARITY: Belongs to the arginase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6D0231978AC1B977 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 1;
Pred. No. 1.4;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1988 (Rel. 08, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Arginase 1 (EC 3.5.3.1) (Liver-type arginase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34808 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 VIWVDAHTDINTPLT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
126
128
128
232
232
234
323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARGI RAT
P07824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
ARGI_RAT
       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAY REPORT OF THE STATE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
```

3 33

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE-81012133; PubMed=6774258;
Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
"Two types of somatic recombination are necessary for the generation
                                                                                                               MEDLINE=81012133; PubMed=6774258; Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.; Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.; "Two types of somatic recombination are necessary for the generation "Two types of immunoglobulin heavy-chain genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 1; Length 115;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION PJ14.
IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 115 IG HEAVY CHAIN V REGION FC
20 >115 IG-LIKE.
115 AA; 12447 MW; 7569DD4A4843D500 CRC64;
                                                                                                                                                                        Nature 286:676-683 (1980).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                               PIRI, A02095; HVMS14.
PIR; A02095; HVMS14.
PBB; LA7N; 29-APR-98.
PBB; LA7P; 29-APR-98.
PBB; LG7H; 17-JAN-01.
PBB; LG7H; 17-JAN-01.
PBB; LG7H; 17-JAN-01.
PBB; LG7H; 17-JAN-01.
PBB; G7G; 17-JAN-01.
PBG; G7G; 17-JAN-01.
PBG; G7G; 17-JAN-01.
PROSITE; SRO0497; IG9; 1.
PROSITE; PSSO835; IG_LIKE; 1.
PROSITE; PSSO835; IG_LIKE; 1.
PROSITE; PSSO835; IG_LIKE; 1.
10-OCT-2003 (Rel. 42, Last annotation update) Ig heavy chain V region PJ14 precursor. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region MOPC 141 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.4%;
                                                                                                                                                                                                                                                                                                                                      EMBL; V00767; CAA24148.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VIWSGGNTDYNT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 MIWGDGSTDYNS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV43 MOUSE
P01819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
PROSITE; PS00148; ARGINASE 2; 1.

PROSITE; PS01053; ARGINASE 3; 1.

Urea cycle; Arginine metabolism; Hydrolase; Manganese; 3D-structure.

METAL 101 ANGANESE 1.

METAL 124 124 MANGANESE 1 AND 2.

METAL 126 MANGANESE 2.

METAL 128 MANGANESE 1.

METAL 232 ANANGANESE 1.

METAL 234 MANGANESE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 1; Length 323; Pred. No. 1.4; 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34973 MW; 5A92CB0931F9A053 CRC64;
                                                                                                                                -> P (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 01, Created)
(Rel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . STANDARD;
                                                                                                                                               111288447046888
9999444999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179
194
199
206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HV44 MOUSE
P01820;
21-JUL-1986
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TURN
TURN
SEQUENCE
                                                          METAL
METAL
METAL
METAL
METAL
CONFLICT
STRAND
                                                                                                                                                            TURN
HELIX
TURN
HELIX
TURN
STRAND
STRAND
STRAND
TURN
STRAND
HELIX
TURN
STRAND
HELIX
HELIX
HELIX
TURN
TURN
TURN
TURN
HELIX
TURN
HELIX
STRAND
HELIX
HELIX
HELIX
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAND
HELIX
TURN
STRAND
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
HV44 MOUSE
ID HV44 MC
AC P01820;
DT 21-JUL-
DT 21-JUL-
```

ö

```
Query Match
                                                                                                                                                                                                    Matches
        *********
                                                                                                                                                                                                                                     ò
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Boinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
of complete immunoglobulin heavy-chain genes.";
Nature 286:676-683 (1980).
-!- MISCELLANDOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
DIFFERENTIATED GENE ISOLATED FROM A WYELOMA THAT SECRETES IGG2B.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=St. Lawrence 74 / St 74 / ORS 6A;
MEDLINE=87228330; PubMed=3035337;
Nelson M.A., Macino G.;
Structure and expression of the overlapping ND4L and ND5 genes of Neurospora crassa mitochondria.";
Mol. Gen. Genet. 206:307-317(1987).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrion.
Bukaryota, Pungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION MOPC 141. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.4%; Score 47; DB 1; Length 144; 63.6%; Pred. No. 1.8; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               715 AA.
                                                                                                                                                                                                                            EMBL, V00768; CAA24149.1; -. PRR, A02094; G2MS14.
HSRSP, POL1825; 7FB.
HIGENPEO; IPRO07110; InterPro; IPR003596; Ig_v.
PEan; PR0047; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
IMMLOGIObulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X05115, CAB37187.1; -. PIR; S10843; S10843. InterPro, IPR003918; NADHub_oxred4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 IWGNGSTDYNS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IMSGGNIDYNT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUSM NEUCR
P05510;
                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                IGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
NUSM NEUCR
     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
```

```
MEDLINE-20196006; PubMed=10731132;

XR MEDLINE-20196006; PubMed=10731132;

Adama M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adama M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

Adama M.D., Celniker S.E., Holtards S., Ashburner M., Henderson S.M.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A cherry J.M., Doug E.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Upstream sequences of dosage-compensated and non-compensated alleles of the larval secretion protein gene Sgs-4 in Drosophila."; Chromosoma 96:1-7(1987).
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Canton-S;
MEDLINE=92120020; PubMed=1769273;
Furia M., Digilio F.A., Artiaco D., D'Avino P.P., Cavaliere D.,
Polito L.C., "Molecular organization of the Drosophila melanogaster Pig-1 gene.";
Chromosoma 101:49-54(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIGI_DROME STANDARD;
PIGI_DROME STANDARD;
PSC6021, 076514; 024519; 0904T3;
01-MAY-1992 (Rel. 22, Created)
16-OCT-2001 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Pre-intermoult gene-1 protein precursor (Gland specific protein).
PIGI OR PIG-1 OR GSG OR EG:96G10.1 OR CG10790.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Bukaryota: Metazoa, Arthropoda; Haxapoda; Insecta; Pterygota;
Neoprera: Endoprerygota; Diptera: Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                 Score 46; DB 1; Length 715; Pred. No. 14; 4; Indels 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Gregon.R.
Bolshaw V., Borkova D., Minana B., Kafatos F.;
Submitted (UUN-1998) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR003916; NADHub_oxred5.
InterPro; IPR001750; Oxidored q1.
InterPro; IPR001516; Oxidored q1.
InterPro; IPR001516; Oxidored q1.
Pfam; PF00561; oxidored q1; 1.
Pfam; PF00562; oxidored q1; 1.
PRINTS; PR01434; NADHDHGNASE5.
PRINTS; PR01437; NUOXDRDTASE4.
Oxidoreductase; NAD; UDiquinone; Mitochondrion.
SEQUENCE 715 AA; 79817 MW; CFAAF0F45FPAAC277 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAINS-Gregon-R, Karenas, and Samarkand;
MEDLINE-88136816; PubMed=3125018;
Hofmann A., Korge G.;
                                                                                                                                                                                                                                      52.3%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                              |:|: || || |:
185 VLWTLGNLDYATVFS 199
                                                                                                                                                                                                                                                                                                                                1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                          Local Similarity 53.3
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [4]
SEQUENCE FROM N.A.
```

354 AA.

STANDARD;

Thu Oct 14 09:36:58 2004

RESULT 13 ARG2_MOUSE

```
MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
A Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harvey D.A., Heaman T.J., Hearnandez J.R., Houck J.,
A Harris N.L., Harvey D.A., Howland T.J., Wei M.-H. Ibegwam C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Vulp D., Lai Z.,
Lasko P., Lei Y., Levelsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
A Mattei B., McIntosh T.C., McLeod M.P., Moshrefi A.,
A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saudes R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Shue B.C., Schadling A.C., Stapleton M., Strong R., Sun E.,
A Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Milliams S.M., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Horley K.C., Mu D., Yang S., Yao Q.A.,
A Cheng X.H., Myers E.W., Zhong W., Zhou X., Zhu S., Zho X., Smith H.O.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A The genome sequence of Drosophila melanogaster.",
A Gribs C. A., Mers P. M., Prop. M., Melanogaster.",
A Gribs C. A., Mers P. M., Melanogaster.",
A Gribs C. A., Mers P. M., Melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILSDING, IN KEF. 2).
KKASNNNSNRRRNNSRRG -> RRHPTTTGAGTTIPGG
VVRAKOWYETTTTGLY (IN REF. 1 AND 2).
4DEB6346D6713841 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNNKKRANŠNNNRKERAŠNNNNKKKASNNNSNRRRNNNSRR
RG -> TTTRRGPTATTIAKGGRPTTTIKRRHPTTTAQAQE
QQFQEAWLERKWLKQQLHVDYMHNKYFFCS (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRE-INTERMOULT GENE-1 PROTEIN.
ALA/ASP/THR-RICH.
ARG/ASN/TS-RICH.
3 X 6 AA TANDEM REPEATS OF S-S-A-D-S-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: Not known.
-i- TISSUE SPECIFICITY: Low amounts in first to third instar larvae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D -> DSSADSD (IN REF. 2 AND 4).
I -> R (IN REF. 1).
I -> T (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.1%; Score 45; DB 1; Length 168; 66.7%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          salivary glands.
-!- DEVELOPMENTAL STAGE: Throughout the larval period.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M24138; AAA28893.1; -.
EMBL; X15760; CAA33767.1; -.
EMBL; ALO24484; CAA19669.1; -.
EMBL; AE003427; AAF45659.1; -.
Flybase; FBGN003086; Pigl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 AA; 18142 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal; Repeat.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: Arginine degradation via the urea cycle; first step. -!- SUBUNIT: Homotrimer (By similarity). -!- SUBCELLULAR LOCATION: Mitochondrial. -!- SIMILARITY: Belongs to the arginase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/60; TISSUE=Kidney;
MEDLINE=99032597; PubMed=9814991;
Morris S.M. Jr., Kepka-Lenhart D., Chen L.C.;
"Differential regulation of arginases and inducible nitric oxide synchase in murine macrophage cells.";
Am. J. Physiol. 275:E740-E747(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthesis (By similarity).
CATALYTIC ACTIVITY: L-arginine + H(2)0 = L-ornithine + urea.
COFACTOR: Manganese.
                                                                      01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginase II, mitochondrial precursor (EC 3.5.3.1) (Non-hepatic arginase) (Kidney-type arginase).
                                                                                                                                                                                                                                                                                                                                                                                                                     Iyer R.K.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00491; arginase; 1.
PRINTS; PR00116; ARGINASE.
TIGREPAMS; TIGRO1229; roc2
PROSITE; PS00147; ARGINASE 1; 1.
PROSITE; PS01053; ARGINASE 2; 1.
PROSITE; PS01053; ARGINASE 3; 1.
Urea cycle; Arginine metabolism; Hydrolase; Manganese; Transit peptide; Mitchchondrion.

1. 22 MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF04596; AAC7846.1; EMBL; AF04596; AAC78460.1; EMBL; AF04595; AAC78460.1; COUNED. EMBL; AF044596; AAC78460.1; JOINED. EMBL; AF044596; AAC78460.1; JOINED. EMBL; AF04596; AAC78460.1; JOINED. EMBL; AF045969; AAC78460.1; JOINED. EMBL; AF045969; AAC78460.1; JOINED. EMBL; AF0459695; AAC78460.1; JOINED. EMBL; AF0459695; AAC78460.1; JOINED. EMBL; AF0459695; AAC78460.1; JOINED. EMBL; AAC7860695; AAC78460.1; JOINED. EMBL; AAC7860695; AAC78660.1; AAC7860.1; AAC7860.1; AAC7860.1; AAC7860.1; AAC7860.1; AAC7860.1; AAC7860.1; AAC7860.1; 
                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=C57BL/6; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U90886; AAC22548.1; -.
                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129/Sv;
```

```
1.
          SOT THE STATE OF THE SOLUTION OF THE STATE OF THE SOLUTION OF THE STATE OF THE SOLUTION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its concent to modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Wister, TISORE-Small intestine,

X GEORGALY TISORE-Small intestine,

A GOLO T. V. SONOKI T., Magasaki A., Terada K., Takiguchi M., Mori M.;

A GOLO T., SONOKI T., Magasaki A., Terada K., Takiguchi M., Mori M.;

"Molecular cloning of CDNA for nonhepatic mitochondrial arginase

(arginase II) and comparison of its induction with nitric oxide

T synthase in a murine macrophage-like cell line.";

FEBS Lett. 395:119-122 (1996).

- I- FUNCTION: May play a role in the regulation of extra-urea cycle

arginine metabolism and also in down-regulation of nitric oxide

synthesis (By similarity).

- I- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-ornithine + urea.

- C-I- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-ornithine + urea.

- C-I- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-ornithine + urea.

- C-I- CATALYTIC ACTIVITY: L-arginine degradation via the urea cycle; first step.

- SUBUNIT: Homotrimer (By similarity).

- SUBUNIT: Homotrimer Companial.

- SUBUNITY: Belongs to the arginase family.
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (kai).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARG2_RAT STANDARD; PRT; 354 AA.
008701; P97539;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginase II, mitochondrial precursor (EC 3.5.3.1) (Non-hepatic arginase) (Kidney-type arginase)
                                                                                                                                                                                                                                                                                                    51.1%; Score 45; DB 1; Length 354; 53.3%; Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iyer R.K.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                        B372DF68A19473F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
ARGINASE II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement ((
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS, PR00116; ARGINASE.
TIGRFAMS; TIGR01229; rocF arginase; 1.
PROSITE; PS00147; ARGINASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=Sprague-Dawley; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR006035; Arg agm form.
Interpro; IPR005924; Arginase.
Pfam; PF00491; arginase; 1.
                                                                                                                                                                                                                                    38878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U90887; AAC22580.1; -. EMBL; D86928; BAA13183.1; -. HSSP; P07824; 1D3V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 VIWVDAHADINTPLT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 87-168 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                            Conservative
   354
120
143
145
147
251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
23
120
143
145
147
251
354 AA;
                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDA N N DDA N DDA N DDA N N DD
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: First detected in neurula (stage 16/17). Highest levels in whole tadpole found around stage 47/48. In the intestine, increased levels are found during metamorphosis (stages 58-64). Low levels expressed in hindlimb until stage 66 after which, levels dramatically increase. In the tail, a constant high level of expression is found throughout metamorphosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arginase genes during amphibian metamorphosis.";

1. Biol. Chem. 269:2538-25334(1994).

1. FUNCTION: As well as its role in the urea cycle, may be involved in tissue remodeling.

1. CATALYTIC ACTIVITY: L-arginine + H(2)0 = L-ornithine + urea.

1. COPACION: Manganese (By similarity).

1. PATHWAY: Arginine degradation; first step.

1. SBUNIT: Homotrimer (By similarity).

1. TISSUE SPECIFICITY: Expressed at differing tadpole stages in tail, intestine, hindlimb and trunk region. Most abundant in tadpole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (BY SIMILARITY) SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB=Intestine; who wed=7929226; who burnes=95014323; who were the steaten b., Shi Y.-B.; "Thyroid hormone-dependent differential regulation of multiple "Thyroid hormone-dependent differential regulation of multiple contents the steatest of the steates
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> V (IN REF. 2).
-> L (IN REF. 2).
BC03E6BC99B29B8C CRC64;
PROSITE; PS01053; ARGINASE 2; 1.
Urea cycle; Arginine metabolism; Hydrolase; Manganese;
Transit peptide; Mitochondrion.
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the arginase family.
                                                                                                                                                                                                                                                                                                                           ARGINASE II.

MANGANESE I (BY S
MANGANESE I IN REF I IN S
MANGANESE I IN REF I IN MANGANESE I IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 1;
Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Arginase, non-hepatic 1 (EC 3.5.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ^ ^ ^ ^ ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38640 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 VIWVDAHADINTPLT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VIWSGGNIDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
NCBL_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
Les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARG1 XENLA
Q91553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
METAL
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARG1_XENLA
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation-
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
51.1%; Score 45; DB 1; Length 360;
Best Local Similarity 53.3%; Pred. No. 9.5;
Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                              EMBL, U08406; AAA56891.1; --
PIR, I51663; I51663.
RISSP: P07824; 1D3V.
InterPro; IPR005924; Arginase.
InterPro; IPR005924; Arginase.
PEAM; PR00491; arginase; 1.
PRINTS; PR00116; ARGINASE.
ITCRFAMS; TIGRO1229; rocF arginase; 1.
PROSITE; PS00147; ARGINASE 1; 1.
PROSITE; PS00149; ARGINASE 2; 1.
PROSITE; PS00149; ARGINASE 2; 1.
Wiltigene family.
Multigene family.
Margal.
Marg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 MA
145 MA
147 MA
149 MA
253 MA
39155 MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
SEQUENCE
```

Search completed: October 6, 2004, 16:30:24 Job time: 11.2105 secs

g ò

ö

Gaps

ö

Q826k9 streptomyce
Q97jz8 streptomyce
Q97jz8 streptomyce
Q97me6 clostridium
Q871g7 mus musculu
P73589 synechocyst
Q87x5 clostridium
Q82tq2 pyrobaculum
Q8339 pyrococcus
O5839 pyrococcus
O5839 pyrococcus
O5839 pyrococcus
Q9201 pyrococcus
Q9a20 caulobacter
O56785 staphylococc
Q8455 verticilliu
Q8a20 bacteroides
O42800 aspergillus
Q8j0p4 aspergillus
Q7447 bacteriopha
Q92w51 rhizobium
Q8ei47 shewanella

042795 collectric 099012 trichoderma 0909098 leishmania 0864n2 vibrio vuln 0865 streptococc 089h8 bradyrhizob 09914 mus musculu 089114 drosophila

OM protein

Run on:

Sequence:

Searched:

Database

```
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20036896, PubMed=10567266,
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Mincon K.W., Fleischmann R.D.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the radioresistant bacterium Deinococcus radiodurans \mathrm{Rl.}\,";
                                                                                                                                                                                                                                                                                                                                                                                Deinococcus radiodurans.
Bacteria, Deinococcus-Thermus, Deinococci; Deinococcales;
Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001922; AAF10226.1; -.
PIR; H75493; H75493.
HSSP; P53609; 2CEV.
TIGR; DR0651; -.
GO; GO:0004053; F:arginase activity; IEA.
GO; GO:0005527; P:arginine catabolism; IEA.
InterPro; IPR065924; Arginase.
InterPro; IPR06924; Arginase.
PFAm: PF0441; arginase.
                                                                                                                                                                                                                                                                                                                      301 AA
                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006035; Arg_agm_form.
Pfam; PF00491; arginase; 1.
PRINTS; PR00116; ARGINASE.
TIGRFAMS; TIGR01229; rocF_arginase; 1.
                          097ME6
081107
081107
081702
081313
081313
081313
091701
091734
091734
0917407
0017407
0017407
0017407
0017407
0017407
0017407
Q826K9
Q9RJZ8
Q8NKF9
                                                                                                                                                                                                             Q8D4N2
Q8K6J5
Q89HH8
Q99NG4
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                             117
116
116
116
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 286:1571-1577(1999).
                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
PRELIMINARY;
                                                                                              50.6
                                                                                                                Arginase.
DR0651.
                                                                                                                                                                                                                                                                                                                                Q9RWL5;
                                                                                                                                                                                                                                                                                                                     Q9RWL5
                                                                                                                                                                                                                                                                                                     RESULT 1
Q9RWL5
                                                                                                                                                                                                                                                                                                                        09rwl5 deinococcus
09ltn6 tupaia herp
08shp7 trichoderma
08hp3 bo homo sapien
08yxd0 anabaena sp
095jc8 sus scrofa
08ter2 homo sapien
08ter2 homo sapien
08tyr4 mus musculu
08hhc6 cryphonectr
08haus cryphonectr
08haus cryphonectr
08hd2 cryphonectr
                                                        October 6, 2004, 16:23:13 ; Search time 50.2632 Seconds (without alignments) 94.160 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                        1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                       summaries
                                          protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FWL5
Q91TN6
Q8FB77
Q9FXD0
Q8FXD0
Q95JC8
Q8TF72
Q80V14
Q91X92
Q8HHC6
Q8HHC6
Q89H72
                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                               sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_numan:*
sp_numan:*
sp_nnvertebrate:*
sp_mnc:*
                                                                                                                                                                                                                                                                                                                                                                                  sp_unclassified:*
                                                                                                                                                                                                                                                                                                                        sp_organelle:*
sp_phage:*
sp_phage:*
sp_rodent:*
sp_virus:*
sp_virus:*
                                                                                                             1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                  sp_bacteriap:*
                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                            US-09-635-974A-4
88
                                                                                                                                                                                                                                                                                                                                                                                                            archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rvirus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
DB
                                                                                                                                                                                                                                                       SPTREMBL 25:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       %
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                          ı
```

Q97dn6 clostridium Q872j1 neurospora Q97ym6 sulfolobus

Q97DN6 Q872J1 Q97YM6

16 3

48978878844

Result Š.

```
Chambergo F.S., Bonaccorsi E.D., Ferreira A.J.S., Ramos A.S.P.,
Chambergo F.S., Bonaccorsi E.D., Ferreira A.J.S., Ramos A.S.P.,
Chambergo F.S., Bonaccorsi E.D., Farah J.P.S., El-Dorry H.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF447590; AAL74164.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0006137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016120; P:mitochondrial electron transport, NADH to u. .; IEA.
"Elucidation of the Metabolic Fate of Glucose in the Filamentous Fungus Trichoderma reesel Using Expressed Sequence Tag (EST) Analysis and cDNA Microarrays.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.0%; Score 51; DB 8; Length 692; 53.3%; Pred. No. 10; 3; Indels ive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00361; oxidored_q1; 1.—Pfam, PF00361; oxidored_q1 N; 1.
PRINTS; PR01434; NADHDHGNASES.
NAD; Oxidoreductaee; Ubiquinone; Mitochondrion.
SEQUENCE 692 AA; 77171 MW; 89821FAAFCBA6C81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0004053; Franginase activity; IEA.
GO; GO:0003824; Frantalytic activity; IEA.
GO; GO:0006527; Pranginine catabolism; IEA.
InterPro; IPR005924; Anginase.
InterPro; IPR006035; Ang agm_form.
Ffam; PF00491; anginase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PROOII6; ARGINASE.
TIGREAMS; TIGR01229; rocF arginase; 1.
PROSITE; PSO0147; ARGINASE 1; 1.
SEQUENCE 236 AA; 25356 MW; 79F02C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                InterPro; IPR003916; NADHUD oxreds.
InterPro; IPR001750; Oxidored_g1.
InterPro; IPR001516; Oxidored_g1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 ILWSLGNLDYSTVFS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similar to arginase, liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 53.3
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BS50;
Q9BS50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BS50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bahr U., Darai G.; "Analysis and Characterization of the Complete Genome of Tupaia (Tree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE=21950703; PubMed=11825887;
Chambergo F.S., Bonaccorsi E.D., Ferreira A.J.S., Ramos A.S.P.,
Ferreira Junior J.R., Abrahao-Neto J., Farah J.P.S., El-Dorry H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion.

Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocrecmycetidae; Hypocreales; Hypocreaceae; Hypocrea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 58.0%; Score 51; DB 12; Length 575; Local Similarity 57.1%; Pred. No. 8.5; es 8; Conservative 2; Mismatches 4; Indels
                                                                                                                        Score 53; DB 16; Length 301; Pred. No. 1.9;
                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF281817; AAK57101.1; -...
GO, GO:0019031; C:viral envelope; IEA.
InterPro, IPR00257; Herpes env.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01673; Herpes env; I.
SEQUENCE 575 AA; 63743 MW; BE62BEF35166825D CRC64;
                                                                              301 AA; 32339 MW; 9DDD18F99E744682 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tupaia herpesvirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         692 AA
                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADH-ubiquinone oxidoreductase chain 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trichoderma reesei (Hypocrea jecorina).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=2;
MEDLINE=21211637; PubMed=11312357;
             PROSITE; PS00147; ARGINASE_1; 1. PROSITE; PS00148; ARGINASE_2; 1. Complete proteome. SEQUENCE 301 AA; 32339 MW; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rew) Herpesvirus.";
Virol, 75:4854-4870(2001).
                                                                                                                           69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 VWSGTNVFFNTPLT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                               118 VIWVDAHTDYNTP 130
                                                                                                      Query Match
Best Local Similarity 69.4%
Best Local Similarity
Gonservative
                                                                                                                                                                                                                1 VIWSGGNTDYNTP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Betaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8SHP7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8SHP7
                                                                                                                                                                                                                                                                                                                                                                          9NT160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                         RESULT 2
091176
091776
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
091770
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170
09170

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
Q8SHP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S KW DR
                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

ö

Gaps

. 0

SEQUENCE FROM N.A. Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator(TM) System Donor Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Length 236; TISSUE=Skeletal muscle; Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL, BC005321, AAH05321.1, -. EMBL, BT006741, AAP35387.1, -. 79F02C69B700AB67 CRC64; (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 25, Last annotation update)

ó

Gaps

RESULT 5

ACCOS ON THE STANT OF THE STANT

à

g

```
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FACTOR N.A..

SUBMITTED (JAN-2002) to the EMBL/GenBank/DDBJ databases.

B MBC: 00004053; Fearginase activity; IEA.

GO; GO:0003824; F: Cartalytic activity; IEA.

GO; GO:0003824; F: Cartalytic activity; IEA.

GO; GO:000527; P: Rarginase actabolism; IEA.

R InterPro; IPR006524; Arginase.

R InterPro; IPR006524; Arginase.

R PRINTS; PR00112, Arginase; I.

R PRINTS; PR00112, Arginase; I.

R PROSITE; PS00147; ARGINASE 1; I.

R PROSITE; PS00149; ARGINASE 2; I.

R PROSITE; PS00148; ARGINASE 2; I.

R PROSITE; PS01048; ARGINASE 3; I.

R SEQUENCE 330 AA; 35664 MW; 5747D414E8741D7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.8%; Score 50; DB 4; Length 330; 60.0%; Pred. No. 6.6; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                      Length 322;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                 Hydrolase.
SEQUENCE 322 AA; 35018 MW; D99FB071CB916B2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JOCT-2003 (TrEMBLrel. 25, Last annotation update)
Arginase type I erythroid variant.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Arginase 1, liver.
                                                                                                                                                                                                                                                                                                               Query Match 56.8%; Score 50; DB 6; Best Local Similarity 60.0%; Pred. No. 6.4; Matches 9; Conservative 1; Mismatches :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 AA.
                                           PRINTS; PROO116; ÅRGINASE.
TIGRRAMS; TIGRO1229; TOCF arginase; 1.
PROSITE; PSOO147; ARGINASE 1; 1.
PROSITE; PSO1048; ARGINASE 2; 1.
PROSITE; PSO1053; ARGINASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CZECH II; TISSUE-Breast tumor;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 VIWVDAHTDINTPLT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 VIWVDAHTDINTPLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VIWSGGNTDYNTPFT 15
          Pfam; PF00491; arginase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q80VI4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q80VI4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
Q8TE72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTRACTOR OF CO
          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W MEDLINE-21595285; PubMed=11759840; Kuritz T., Sasamoto S., Kanteko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Akatanabe A., Iriguchi M., Ishikawa A., Kawashima X., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki M., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Asuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., R. Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.", BMBL; Apo03585; BAB73241.1; -. BMBL; Apo03585; BAB73241.1; -. BMBL; Apo03585; Al1966.

BR PIK, Al1966, Al1966.

CO, GO:0005215; Fitransporter activity; IEA. GO; GO:0005215; Fitransporter activity; IEA. GO; GO:0005215; Fitransporter activity; IEA. GO; GO:0005215; Bab_Transporter activity; IEA. GO; Fitransporter acti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Arginase I EC 3.5.3.1).
Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.8%; Score 50; DB 16; Length 288; 53.3%; Pred. No. 5.7; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALL1284.
Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 AA; 30913 MW; AE7C2E0D454E41FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Permease protein of ABC transporter.
                                                                                                                                                                                                                                                                                                                                                       288 AA.
       Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 AA.
                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                   PRT;
Best Local Similarity 60.0%;
Matches 9; Conservative 1
                                                                                                                                                                      120 VIWVDAHTDINTPLT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 LIWGGRNONYNLPIT 128
                                                                                                     1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.3%
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q95JC8
Q95JC8;
                                                                                                                                                                                                                                                                                                                                                                                    28YXDO;
                                                                                                                                                                                                                                                                                                                                                OBYXDO
```

. 0

Gaps

RESULT 6

à g

```
SEQUENCE FROM N.A.
STRAIN=I-3, I-4, I-9, I-10, and I-12b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR003916; NADHub oxreds.
Interpro; IPR001750; Oxidored_q1.
Interpro; IPR001516; Oxidored_q1.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00361; oxidored q1; 1.
Pfam; PF00662; oxidored q1 N; 1.
PRINTS; PR01434; NADHDHGNASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 ILWSLGNLDYATVFS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55...
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ubiquinone; Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=I-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBHAU8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8HAU8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8HAU8
      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE PLANT OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
Submitted (WAR-2003) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0004053; F:atalinase activity; IEA.

GO; GO:0003824; F:catalytic activity; IEA.

R GO; GO:000527; P:arginine catabolism; IEA.

R GO; GO:000627; P:arginine catabolism; IEA.

R InterPro; IPR005035; Arginase.

R InterPro; IPR006035; Arginase.

R PEAM; PF00491; arginase; 1.

R PRINTS; PR00116; ARGINASE 1: 1.

R PROSITE; PS00147; ARGINASE 1: 1.

R PROSITE; PS00148; ARGINASE 2: 1.

R PROSITE; PS00148; ARGINASE 2: 1.

R PROSITE; PS00153; ARGINASE 2: 1.

R PROSITE; PS00153; ARGINASE 3: 1.

R PROSITE; PS00153; ARGINASE 3: 1.

R PROSITE; PS00153; ARGINASE 3: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 56.8%; Score 50; DB 11; Length 335; Best Local Similarity 60.0%; Pred. No. 6.7; Matches 9; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.7%; Score 49; DB 11; Length 482; 66.7%; Pred. No. 15; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cryphonectria parasitica (Chesnut blight fungus) (Endothia parasitica).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC011181, AAH1181.1;
PIR; F33932; F33932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00047; ig; 4. ——
Pfam, PF00047; ig; 4. ——
PROSITE; PS00835; IG_LIKE; 4. 
PROSITE; PS00290; IG_MHC; 2. 
Hypothetical protein. 
SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       091X92 PRELIMINARY; PRT; 482 AA. 091X92; 011X92; TEBMELrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DCT-2003 (TrEMBLrel. 19, Last annotation update) Hypothetical protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MDR-2003 (TrEMBLrel. 23, Created)
01-MDR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH-ubiquinone oxireductase subunit 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 VIWVDAHTDINTPLT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66...
8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VIWSGGNTDYNT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 VIWTGGVTNYNS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBHHC6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     овнисе
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
08HHGC
10 08HHGC
AC 08HHGC
DT 01-MAJ
DT 01-MAJ
DT 01-MAJ
DT 01-MAJ
OS NADH-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
(91x92
(10 091x)
(92 091x)
(92 091x)
(93 091x)
(93 091x)
(94 091x)
(95 091x)

             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          임
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                   A Gobbi E.;

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF456841; AA014107.1; -.;

EMBL; AF456841; AA014107.1; -.;

EMBL; AF456841; AA014107.1; -.;

EMBL; AF456841; AA014107.1; -.;

R GO; GO:0005130; C:mitcochondrial electron transport, NADH to u. .;

R GO; GO:0006120; P:mitcochondrial electron transport, NADH to u. .;

R GO; GO:0006120; P:mitcochondrial electron transport, NADH to u. .;

R InterPro; IPR001516; Oxidored_q1.

R InterPro; IPR001516; Oxidored_q1.

R Pfam; PF00662; Oxidored_q1.

R Pfam; PF00662; Oxidored_q1.

R PRINTS; PR01434; NADHDHGNASE5.

W Ubiquinone; Mtcchondrion.

T NON TER 136 136

SEQUENCE 136 AA; 15244 MW; F9ACEEBBI38F3D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF456819; AAO14104.11; --
EMBL, AF456840; AAO14106.1; --
EMBL, AF456841; AAO14108.1; --
EMBL, AF456843; AAO14110.1; --
EMBL, AF456844; AAO14111.1; --
EMBL, AF456849; AAO14111.1; --
EMBL, AF456849; C. mitcohondrion; IEA.
GO, GO:00005137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
GO; GO:0006120; P:mitcohondrial electron transport, NADH to u...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Diaporthales; Valsaceae;
Cryphonectria-Endothia complex; Cryphonectria.
Mitochondrion.

Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Diaporthales; Valsaceae; Cryphonectria-Endothia complex; Cryphonectria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crownonectria parasitica (Chesnut blight fungus) (Endothia parasitica).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 8; Length 136; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gobbi E.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH-ubiquinone oxireductase subunit 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.5%; SCc. No. 5...,
53.3%; Pred. No. 5...,
".ve 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 AA.
```

us-09-635-974a-4.rspt

```
:|| |||:| ||
520 MIWFNGNTNYVTP 532
                                                 (1)
SEQUENCE FROM N.A.
           NCBI_TaxID=5116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium.
NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            097DN6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9NG760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
Q872J1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    997DN6
           NA REPRESENTATION OF THE PROPERTY OF THE PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  업
                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kanbro T., Nakamurra Y., Sato S., Minamisawa K., Uchiumi T.,
Kanbro T., Nakamura Y., Idesawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watenabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005957; BAC51387.1; -.
GO; GO:0004053; F:arginase activity; IEA.
GO; GO:0003824; F:catalyric activity; IEA.
GO; GO:0005824; P:catalyric activity; IEA.
InterPro; IPR005924; Arginase.
InterPro; IPR005924; Arginase.
DEFA. DEFA. DEFA. Arginase.
DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. DEFA. D
                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parasitica).
Mitochondrion.
Mitochondrion.
Eukaryota; Parizomycotina; Sordariomycetes; Sordariomycetidae; Diaporthales; Valsaceae; Cryphonectria-Endothia complex; Cryphonectria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Match 54.5%; Score 48; DB 16; Length 325; Local Similarity 53.3%; Pred. No. 14; es 8; Conservative 2; Mismatches 5; Indels
                                                                    Query Match 54.5%; Score 48; DB 8; Length 136; Best Local Similarity 53.3%; Pred. No. 5.2; Matches 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cryphonectria parasitica (Chesnut blight fungus) (Endothia
   15204 MW; F9B296B6EB99BD99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 AA; 35660 MW; 92964D631E8D2BCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created) Last sequence update) Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
NADH-ubiquinone oxireductase subunit 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00147; ARGINAE ; 1.
PROSITE; PS00148; ARGINASE 2; 1.
PROSITE; PS01053; ARGINASE 3; 1.
Complete proteome 325 AA; 35660 MW; 92
                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 VLWLDAHADYNTPET 145
                                                                                                                                                                                                                  1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VIWSGGNIDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00491; arginase; 1
PRINTS; PR00116; ARGINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arginase.
   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBHHD2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q89H72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8HHD2
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
Q89H72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
   S
                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
ö
GODDIE.;
GODDIE.;
GODDIE.;
GODDIE.;
EMBL, AF45603B.; AAO14099.1;
GO, GO,10005739; C:mitochondrion; IEA.
GO, GO,10005739; C:mitochondrion; IEA.
GO, GO,10008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
GO, GO,10008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
InterPro; IPR003918; NADHUD oxred4.
InterPro; IPR001750; Oxidored_G1.
InterPro; IPR001750; Oxidored_G1.
InterPro; IPR001516; Oxidored_G1.
InterPro; IPR001516; Oxidored_G1.
InterPro; IPR001816; Oxidored_G1.
I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAINSATCS 924 / DSM 792 / VKM B-1787;

KR MEDLINE=2139325; PubMed=11466286;

KN MEDLINE=2139325; PubMed=11466286;

RA Gibson Kr. Lee H.M., Dubois J., Hitti J., Wolf Y.I.,

A dubson Kr., Sabathe F., Ooucete-Stamm L., Soucaille P., Daly M.J.,

A Tatusov R.L., Sabathe F., Doucete-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

Teonome sequence and comparative analysis of the solvent-producing

To bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).

R. Br. Br. C97322, C97322.

R. InterPro; IPR003305; CBM CenC.

R. InterPro; IPR003979; Gal_bind_like.

R. Frim: PF02018; CBM_4 9; T.

R. Complete proteome.

SEQUENCE 835 AA; 93561 MW; 35C11C69D587CEFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.5%; Score 48; DB 16; Length 835; 61.5%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72600 MW; 35C99E836E257DBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Probable alpha-arabinofuranosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.5%; Score 48; DB 8;
53.3%; Pred. No. 30;
iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   835 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 ILWSLGNLDYATVFS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ubiquinone; Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VIWSGGNTDYNTP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 53.3
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
```

```
DD Q872J1 PRELIMINARY; PRT; 301 AA.

AC Q872AJ1 PRELIMINARY; PRT; 301 AA.

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 25, Last annotation update)

DE Probable rAsp f 9 allergen.

GN 64C2.250.

CN Neurospora Carasa.

OC EUKaryote; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

NCBI TAXID=5141;

RN [1]

RN SQUENCE FROM N.A.

RA Schultte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,

RA Nyakatura G., Mewes H.W., Mannhaupt G.;

RN [2]

RA Nyakatura G., Mewes H.W., Mannhaupt G.;

RA Schultted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

RN SQUENCE FROM N.A.

RA German Neurospora genome project;

RA Go:0004553; P:nyarolase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO: GO:0004553; P:nyarolase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO: GO:0004553; P:nyarolase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO: GO:0004553; P:nyarolase activity, hydrolyzing O-glycosyl . . .; IEA.

DR RIPERPOS : IPRO00757; Glyco-hydrole:

RN InterPro: IPRO00757; Glyco-hydrole:

SQ SEQUENCE 301 AA: 31771 MW; PCB56E1498A800CZ CRC64;

CUBLY RACHAS SHILL RACHAS SHI
```

Search completed: October 6, 2004, 16:33:47 Job time : 55.2632 secs

1 VIWSGGNTDYNT-PFT 15 : |: || || || || || 229 IAWAGGVTDYTKGPFT 244

g

à

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

October 6, 2004, 16:34:15; Search time 93.4211 Seconds (without alignments) 51.669 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-635-974A-4 88 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 VIWSGGNTDYNTPFT 15 Scoring table: Sequence:

1351062 segs, 321799191 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%. Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUBL.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUBL.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 28, Appl	4 A	'n	m	7	N	Sequence 115,	Sequence 116,	Sequence 117,	Sequence 1	Sequence 119,	Sequence 120,	Sequence 115,	116,	
QI	US-09-798-689-28	US-09-996-954B-4	US-10-374-600-3	US-10-374-531-3	US-10-374-600-2	US-10-374-531-2	US-10-374-600-115	US-10-374-600-116	US-10-374-600-117	US-10-374-600-118	US-10-374-600-119	US-10-374-600-120	US-10-374-531-115	US-10-374-531-116	
DB	10	10	13	15	7,7	15	12	12	12	12	12	13	12	ч	
% Query Match Length	16	16	16	16	18	18	119	119	119	119	119	119	119	119	
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100,0	100.0	100.0	100.0	
Score	88	88	88	88	88	88	88	88	88	88	88	88	88	88	
Result No.	1	7	m	4	Ŋ	9	7	۵	σ	10	11	12	13	14	

Sequence 118, App Sequence 119, App Sequence 120, App Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 24, Appl Sequence 27, Appl Sequence 27, Appl Sequence 28, Appl Sequence 29, Appl Sequence 24, Appl Sequence 26,	44444444444444444444444444444444444444
5 US-10-374-531- 5 US-10-374-531- 5 US-10-374-600- 2 US-10-374-600- 2 US-10-374-600- 2 US-10-374-600- 3 US-10-374-600- 5 US-10-374-531- 5 US-10-374-600- 2 US-10-374-600- 2 US-10-374-600- 2 US-10-374-600- 2 US-10-374-600- 2 US-10-374-600- 2 US-10-374-600- 2 US-10-374-600- 3 US-10-374-600- 5 US-10-374-600- 6 US-10-374-600- 7 US-10-374-600- 8 US-10-374-600- 9 US-10-374-	5 US-10-374-531-2 5 US-10-374-531-2 5 US-10-374-531-3 5 US-09-865-483-13 US-09-865-483-8 2 US-10-239-656-3 2 US-10-239-656-3 2 US-10-682-845-5 2 US-10-389-417-1 2 US-10-452-357-6
11111111111111111111111111111111111111	000000000000000000000000000000000000000
88 8 10000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6.5 86. 6.5 86. 70 79. 70 73. 65 73. 65 73.
0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

```
US-09-199-688-89-28

| Deblication No. US20030103973A1
| Generation No. US20030103973A1
| APPLICANT: Goldstein, Neil I.
| TITLE OF INVENTION: Combined With Radiation and Chemcherapy
| TITLE OF INVENTION: Combined With Radiation and Chemcherapy
| TITLE OF INVENTION: Combined With Radiation and Chemcherapy
| TITLE OF INVENTION: Combined With Radiation and Chemcherapy
| FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
| CURRENT APPLICATION NUMBER: US/09/798,689
| PRIOR FILING DATE: 1997-09-22
| PRIOR FILING DATE: 1997-09-03
| PRIOR FILING DATE: 1997-09-03
| PRIOR FILING DATE: 1995-06-07
| PRIOR FILING DATE: 1994-00-03
| PRIOR FILING DATE: 1994-10-20
| PRIOR FILING DATE: 1994-10-20
| PRIOR FILING DATE: 1994-10-20
| PRIOR FILING DATE: 1994-02-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 88; DB 10; Length 16; Best Local Similarity 100.0%; Pred. No. 1.4e-06; Matches 15; Conservative 0; Mismatches 0; Indels
```

1 VIWSGGNIDYNIPFT 15

ò

Gaps

```
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-10-374-531-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                     US-09-996-954B-4

Sequence 4, Application US/0996954B

Publication No. US20030157104A1

GENERAL INFORMATION:

APPLICANT: Waksal, Harlan W.

TITLE OF INVENTION: Treatment of Refractory Human Tumors

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

FILE REFERENCE: 11245-46605

CURRENT FILING DATE: 0201-11-036

PRIOR APPLICATION NUMBER: 09/840,146

RRIOR FILING DATE: 04-24-2001

PRIOR FILING DATE: 04-24-2001

PRIOR PLILING DATE: 08-13-1999

PRIOR PLILING DATE: 08-13-1999

PRIOR PLILING DATE: 08-14-1999

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DALICALOU. "V. ---
GENERAL INFORMATION:
APPLICANT: IMCLone Systems Incorporated, et al.
APPLICANT: IMCLONE SYSTEMS INCORPORATION FRAGMENTS FOR
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR
INTIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 88; DB 10; Length 16; Best Local Similarity 100.0%; Pred. No. 1.4e-06; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/973,065C FILING DATE: 19-98
APPLICATION NUMBER: PCT/US96/09847 FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982 FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289 FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM compatible
COMPATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILLING DATE: 25-Reb-2003
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Homo sapiens-Rodent Chimera
US-09-996-954B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10374600
Publication No. US20030224001A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VIWSGGNIDYNTPFT 15
1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-374-600-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10374531
Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
ATTLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 88; DB 12;
100.0%; Pred. No. 1.4e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IEM compatible
OPERATING SYSTEM: MS-DOS
SOFTHARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,531
FILLING DATE: 25-P60-2003
CLASSIFCATION: CURNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                               | JENGTH: 15 amino acids | JENGTH: 15 amino acids | TYPE: amino acid | STRANDEDNESS: not relevant | TOPOLOGY: not relevant | MOLECULE TYPE: petide | HYPOTHETICAL: NO | FRAGMENT TYPE: internal | SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-10-374-600-3
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Broadway
                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VIWSGGNIDYNTPFI 15
```

..

```
APPLICANT: Inclone Systems Incorporated, et al. TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPER Diskette 3.5 inch 1.44 Mb storage
COMPUTER: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: Disk compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION TONNOWN-
PRIOR APPLICATION NUMBER: US/08/973,065C
TILING DATE: 19-Mar-1996
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. SOMERVILLE
REGISTRATION NUMBER: 31245/46003
TELEBHONE: (212) 425-7200
TELEBHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 88; DB 15; Best Local Similarity 100.0%; Pred. No. 1.5e-06; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO FRAGMENT TYPE: Internal SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-10-374-531-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                   RESULT 6
US-10-374-531-2
; Sequence 2, Application US/10374531
; Publication No. US20040006212A1
; GENERAL INFORMATION:
APPLICANT: Imclone Systems Inc.
  2 VIWSGGNTDYNTPFT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VIWSGGNIDYNIPFI 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VIWSGGNTDYNTPFT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-10-374-600-115
                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ď
                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: IMCLONE Systems Incorporated, et al.
APPLICANT: IMCLONE AVIBODY AND ANTIBODY FRAGMENTS FOR INTELLIANT THE GFOWTH OF TUMORS
                                                                                                                                          Query Match
100.0%; Score 88; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: IBM compatible
FILING DATE: 25-Feb-2003
CLASSIFICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: DCT/USS6/09847
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: 15-DEC-1995
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 31,995
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELEBCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 88; DB 12;
100.0%; Pred. No. 1.5e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: peptide HYPOTHETICAL: NO HYPOTHETICAL: NO FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 2:
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELBFAX: (212) 425-5288
WATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
                                                                                                                                                                                                                                          1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                   1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                     US-10-374-600-2
                                                                                               US-10-374-531-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-10-374-600-2
                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                     임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

ô

ö

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESUL: 3
US-10-374-600-117
Sequence 117, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
GENERAL INFORMATION:
JAPLICANT: IMCIONE Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INTELLING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 88; DB 12;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN 1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
RRGIGSTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 31,995
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
                                                                CURRENT APPLICATION DATA:

REPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 116:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECTLE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-7200
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSER: Kenyon & Ke
STREET: One Broadway
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 VIWSGGNTDYNTPFT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÚS-10-374-600-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 88; DB 12; Length 119; 100.0%; Pred. No. 1e-05; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // Sequence 116, Application US/10374600
// Publication No. US20030224001A1
// GENERAL INFORMATION:
// APPLICANT: ImClone Systems Incorporated, et al.
// TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INTLE OF INVENTION INHIBITING THE GROWITH OF TUMORS
                                                                                STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
COUNTRY: US
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
COMPUTER: IBM compatible
COMPUTER: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
  INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/374,600 FILING DATE: 25-Feb-2003 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 115: US-10-374-600-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                   ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 115: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 VIWSGGNTDYNTPFT 64
                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-10-374-600-116
```

à g

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                        Query Match 1100.0%; Score 88; DB 12; Length 119; Best Local Similarity 100.0%; Pred. No. 1e-05; Matches 15; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1.

VS-10-374-600-119

Sequence 119, Application US/10374600

Publication No. US20030224001A1

GENERAL INPORMATION:

APPLICANT: Incline Systems Incorporated, et al.

TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INPIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: cUnknown-
PRIOR APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: DCT/US96/09847
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY, DEDOTAL A. SOMERVILLE
NAME: Deborah A. SOMERVILLE
REGISTRATION NUMBER: 31,995
BEGISTRATION NUMBER: 31,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEPAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
                             INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: incernal
SEQUENCE DESCRIPTION: SEQ ID NO: 118:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 119 amino acids
TYPE: amino acid
SYPES: amino acid
SYPEDEDNESS: not relevant
TOPOLOGY: not relevant
WOLECULE TYPE: peptide
HYPOTHETCAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 119:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESS:
STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VIWSGGNTDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 VIWSGGNTDYNTPFT 64
                TELEFAX:
                                                                                                                                                                                                                                                                                          US-10-374-600-118
                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 88; DB 12; Length 119;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 118, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Inficione Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INFIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
FILING DATE: 07-JUN-1996
APPLICATION WUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION
NAME: Deborah A. Somerville
REGISTATION WUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEFRX: (212) 425-7200
TELEFXX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REPERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-10-374-600-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Peb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSES: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VIWSGGNIDYNIPFI 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 VIWSGGNTDYNTPFT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-374-600-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
```

```
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VIWSGGNIDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                                                                     STATE: New York
COUNTRY: US
ZIP: 10004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212)
TELEFAX: (212)
                                                                                                                                                                                                                                                 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-10-374-531-116
                 US-10-374-531-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-374-531-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                               ö
                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                   100.0%; Score 88; DB 12; Length 119; 100.0%; Pred. No. 1e-05; Live 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 88; DB 12; Length 119; 100.0%; Pred. No. 1e-05; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                     Sequence 120, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10004
COMPUTER READABLE FORM:
BEDDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION UNMER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
PILING DATE: 19-MAT-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELEPHONE: (212) 425-7200
TELEPHONE: (212) 425-5288
INFORMATION FOR SEQ ID NO: 120:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid

STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 120:
US-10-374-600-120
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VIWSGGNTDYNTPFT 15
                                                                                                                          1 VINSGGNIDYNIPFT 15
                                                                                                                                                               50 VIWSGGNTDYNTPFT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 VIWSGGNTDYNTPFT 64
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                   Ouery Match
Best Local Similarity
The 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                  RESULT 12
US-10-374-600-120
US-10-374-600-119
                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 116, Application US/10374531

Publication No. US20040006212A1

GENERAL INFORMATION:

APPLICANT: ImClone Systems Incorporated, et al.

IITLE OF INVENTION:

INHIBODY AND ANTIBODY FRAGMENTS FOR INHIBOTY FRAGMENTS FRAGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
Sequence 115, Application US/10374531
Fublication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
ITILE OF INVENTION: ANTIBODY AND ANTIBODY FRAGNENTS
ITILE OF INVENTION: INHIBITING THE GROWTH OF TUMORS;
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESSS:
STREET: ONE Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage CCMPUTER: IBM comparible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 88; DB 15;
100.0%; Pred. No. 1e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIPICATION: CUNKNOWN-
PRIOR APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 07-UW-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UW-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REPERRNGE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 115
```

```
100.0%; Score 88; DB 15; Length 119; 100.0%; Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INTO THE PROPERTY OF THE REGISTRATION NUMBER: 31,995
REPERENCE/DOCKET NUMBER: 31,995
REPERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEPHONE: (212) 425-7200
TELEPHONE: (212) 425-5288
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGENTY TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
                    FILING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UTN-196
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UTN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
  APPLICATION NUMBER: US/10/374,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: October 6, 2004, 17:09:03 Job time : 94.4211 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VIWSGGNIDYNTPFT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 VIWSGGNTDYNTPFT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-374-531-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 88; DB 15; Length 119;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 117, Application US/10374531
Publication No. US20040006212A1
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR
INHIBITING THE GROWTH OF TUMORS
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
CITY: New York
STATE: New York
                                                                                   COMPUTER READABLE FORM:

MEDIUT TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 25-Feb-2003
CLASSIFICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 116: US-10-374-531-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 425-7200
TELEPAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 VIWSGGNTDYNTPFT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-374-531-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ်
```

.. 0

Gaps

.. 0

```
Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Escherichia coli
US-09-865-483-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Appli
Patent No. 5455030
Sequence 3, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Appl
Sequence 8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                            October 6, 2004, 16:24:54 ; Search time 26.5789 Seconds (without alignments) 29.135 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Sequence 60, Sequence 61, Sequence 33, Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33,
Sequence 20,
Sequence 4, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               issued_Patents_AA:*
1: /cgT2_6/ptodata2/iaa/5A_COMB.pep:*
2: /cgT2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgT2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgT2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgT2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgT2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-865-483-13
US-07-634-278-61
US-07-634-278-61
US-08-477-728-37
US-08-477-728-61
US-08-477-728-61
US-08-477-728-61
US-08-477-728-61
US-08-477-728-61
US-08-477-728-61
US-08-477-00-61
US-08-478-00-61
US-08-484-577-61
US-08-484-537-61
US-08-484-537-61
US-08-484-537-61
US-08-484-537-61
US-08-484-537-61
US-08-484-537-61
US-08-484-537-61
US-08-484-537-61
US-08-487-706-33
US-08-487-706-33
US-08-484-537-33
US-08-487-706-33
US-08-68-1648-537-30
US-08-88-337-61
US-08-88-337-333
US-08-88-337-333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-397-411-3
US-08-397-411-4
                                                                                                                                                                                                                                                                                                                                                                       389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                   US-09-635-974A-4
88
1 VIWSGGNTDYNTPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
No.
```

28	54	61	273		US-08-397-411-6	Sequence 6, Appli	
2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	<u>ល់ល ល ល ល ល ល ល ល ល</u> 4.	4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	44 944 1112 122 222 123 101 101	ww40w004+0	08-397-411-7 -08-81-037-66 -09-189-129-3 -08-308-494A-21 -08-881-037-67 -08-190-199A-67 -08-525-539A-61 -08-525-539A-61 -08-525-539A-61	Sequence 7, Appli Sequence 66, Appli Sequence 21, Appli Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli Sequence 36, Appli Sequence 16, Appli Sequence 16, Appli	
0 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 W W W W W W W W	1111 1111 120 120 120			Sequence 6, Applia Sequence 67, Applia Sequence 36, Applia Sequence 4, Applia Sequence 6, Applia Sequence 6, Applia	
					ALIGNMENTS		
RESULT 1 US-09-865-483-13 Sequence 13, A Fatent No. 668 GENERAL INFORM TITLE OF INVE TITLE OF INVE FILE REFERENC CURRENT APPLI CURRENT APPLI CURRENT APPLI CURRENT APPLI CURRENT APPLI CURRENT APPLI CURRENT FILIN FILE REFERENC CURRENT FILIN FILE REFERENC CURRENT FILIN FILE NUMBER OF SEQ SOFTWARE: PAL SEQ ID NO 13 LENGTH: 16 TYPE: PRT ORGANISM: EBI US-09-865-483-13	ULT 1 09-865-483-1 equence 13, equence 14,	SULT 1 Sequence 13, Application US/0986548. Sequence 13, Application US/0986548. Batent No. 6680633. TITLE OF INVENTION: AVAILABLE REGITILE OF INVENTION: AVAILABLE REGITILE OF INVENTION: AVAILABLE REGITILE REFERENCE: 1599-10197P. CURRENT APPLICATION NUMBER: US/09/CURRENT FILING DATE: 2001-03-29 NUMBER OF SEQ ID NOS: 14 SEQ ID NO 13 LENGTH: 16 TYPE: PRT ORGANISM: Escherichia coli -09-865-483-13	ion US/096548 Wook et al. A VARIABLE REG ANTICEN AND A-0197P NUMBER: US/09/2001-03-29 :: 14 ersion 3.1)/09 et ABL ABL EN :: U -03	JON OF THE GENE ENCOI 865,483	MONOCLONAL ANTIBODY AGAINST THE HBV DING THE SAME	v s-81
Query Best L Matche Qy	Query Match Best Local Si Matches 12;	Similarity 85.2; Conservativ	79 85 vativ YNTPF	.58; % 7.8; 14.14	Score 70; DB 4; Length 1 Pred. No. 0.00045; 0; Mismatches 2; Indel	16; :ls 0; Gaps 0;	
RESULT 2 US-09-865-483-8 US-09-865-483-8 Sequence 8, A Sequence 8, A FALTEL INFORM TITLE OF INV.	LT 2 9-865-483-8 quence 8, A quence 8, A quence 8, A quence 7, A TITLE OF INV TITLE	ULT 2	YNAAF ON US/ ON US/ WOOK A VARI ANTIG ANTIG 20197P 114 ersion	14 0980 et e ABLI EN 1 : U%	OF THE MONOCLONAL NE ENCODING THE SAN, 483	ANTIBODY AGAINST THE HBV	. s-s
TYPE	TYPE: PRT	TYPE: PRT ORGANISM: Rechemichia coli			·		

ö

Gaps

ô

Score 70; DB 4; Length 114; Pred. No. 0.0033; 0; Mismatches 2; Indels

```
Score 65; DB 1; Length 119;
Pred. No. 0.018;
                                                                                                                                         GENERAL INFORMATION:
APPLICANT: OTERN, CATY L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: APPLICANT: COELINGH, Natholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTX:

ZIP: 94301

COMPUTER READBLE FORM:

NEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

SOFRATING SYSTEM:

OSFRANTE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/634,278

FILING DATE: 19-DEC-1990

TOTAL OF THE COMPATION:

APPLICATION: APPLICATION:

APPLICATION: APPLICATION:

TOTAL OF THE COMPATION:

APPLICATION: APPLICATION:

TOTAL OF THE COMPATION:

APPLICATION: APPLICATION:

TOTAL OF THE COMPATION:

TOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PATOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INPORMATION:
NAME: Smith, william M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 61, Application US/07634278;
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: OUEBN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
                                                                           Sequence 60, Application US/07634278 Patent No. 5530101
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOWINGER: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.9%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VIWSGGNIDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 VIWSGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-07-634-278-61
                    RESULT 4
US-07-634-278-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Amino acid sequence of the heavy chain of the humanized mik-betal antibody."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB 1; Length 119; Pred. No. 0.018;
                                                                                                                                                                                                    Sequence 10. 5530101

Patent No. 5530101

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: CO. Man Sung

APPLICANT: COLINGH, Kathleen L.

APPLICANT: COLINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOCLOBLINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEARI "TOWNSEARI "ADDRESSEE:

ADDRESSEE: ADDRESSEE:

STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOOTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/634,278

FILING DATE: 19-DEC-1990

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: SMith, William M

REGISTRATION NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:

NAME: SMith, William M

REGISTRATION NUMBER: 11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VIWSGGNTDYNTPF 14
1 VIWSGGNTDYNTPF 14
                                                              50 VIWSGGNTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abbara
STREET: 375 _ (CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein
CCATION: 1..119
OTHER INFORMATION:
US-07-634-278-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CENGTH:
                                                              g
```

.. 0

Gaps

50 VIWSGGSTDYNAAF 63

```
NAME/KEY: Protein
LOCATION: 1.119
OTHER INFORMATION: /note= "Amino acid sequence of the
OTHER INFORMATION: heavy chain of the humanized mik-betal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.9%; Score 65; DB 1; Length 119; 78.6%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-477-728-60

| Sequence 60, Application US/08477728
| Sequence 60, Application US/08477728
| Patent No. 585089
| GENERAL INFORMATION:
| APPLICANT: CUEEN, Cary L. | APPLICANT: SCHNEIDER, William P. | APPLICANT: SCHNEIDER, Harold E. | ITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS | NUMBER OF SEQUENCES: 113 | NUMBER OF SEQUENCES: 113 | NUMBER OF SEQUENCES: | ADDRESSEE: Townsend and Townsend and Crew LLP | STREET: Two Embarcadero Center, 8th Floor | CITY: Palo Alto | STATE: California | STATE: California | COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US /08/477,728
FILING DATE: O'-JUN-1995
CLASSIFICATION NUMBER: US 07/634,278
FILING DATE: US 07/634,278
FILING DATE: US 07/634,278
FILING DATE: US 07/590,274
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 126-E5P-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-E5P-1990
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smath, William M
RESISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2420
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TYPE: Floppy disk
PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 VIWSGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 78.6
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: BINGLE TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-477-728-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 119; 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
          APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/08477728

Patent No. 5585089

GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED INMUNOGLOBLINS NUMBER OF SEQUENCE: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                               CONDITY: US

ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-PES-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FES-1989
ATTORNEY/AGENT INFORMATION:
NAME: SMICH, WAILER MS
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CIYE: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.9%; Score 65; DB 78.6%; Pred. No. 0.01 tive 1; Mismatches
                                                                                                                                                                               379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 VIWSGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 78.6
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                    STREET: 379 Lytton
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-634-278-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-477-728-37
```

g

ó

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/08474040

Patent No. 5693761

GENERAL INFORMATION:
APPLICANT: OC, Man Sung
APPLICANT: ANDOLFI, Niliam P.
APPLICANT: ANDOLFI, Nicholas F.
APPLICANT: ANDOLFI, Nicholas F.
APPLICANT: SELICK, Harold B.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65; DB 1; Length 119;
Pred. No. 0.018;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: TRADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Date |
COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Townsend and Townsend Khourie and Crew
                        FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELECHONE (415) 326-2420
INFORMATION POR SEQ ID NO: 61:
CENGTH: 119 amino acids
TENGTH: 119 amino acids
TENGTH: 119 amino acids
TENGTH: 119 amino acids
TENGTH: 119 amino acids
TOPOLOGY: linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATE.
FILING DATE: 13-FEB-120-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
APPLICATION NUMBER: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VIWSGGNIDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-08-477-728-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-474-040-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 61, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: STATICK, HARVOLD HUMANIZED INMUNOGLOBLINS
TITLE OF INVENTION: IMPROVED HUMANIZED INMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65; DB 1;
Pred. No. 0.018;
                                                                                             CLASSIFICATION D474

PURIOR APPLICATION D474

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

FRIING DATE: 19-DEC-1990

FRIING DATE: 28-DE-1990

FRIING DATE: 28-DE-1990

FRIING DATE: 18-EB-1990

FRIING DATE: 18-EB-1989

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION: NAME: Smith, William M REGISTRATION UNMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICALLONDER: 19-DEC-1>>U
TRING DATE: 19-DEC-1>>U
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
      APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.9%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 VIWSGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 78.6
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-08-477-728-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-477-728-61
```

; 0

```
Length 119;
                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: QUEEN, Cary L.
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
UNDERS OF SECURICES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppd disk
COMPUTER: ISM PC compatible
SOCTAME: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 10-TO-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/310,252
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 13-FEB-1989
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 13-FEB-1989
FRICH APPLICATION NUMBER: US 07/290,975
FRICH APPLICATION NUMBER: US 07/290,975
FRICH APPLICATION NUMBER: US 07/290,975
FRIENDENCHOLOGIET NUMBER: 11823-002600
TELECOMMUTICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                            Score 65; DB 1;
Pred. No. 0.018;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 61, Application US/08474040 Patent No. 5693761 GENERAL INFORMATION:
                 TELECOMMUNICATION INFORMATION:
                                      TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                            73.9%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                        1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 VIWSGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                        single
                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-474-040-60
                                                                                                                                                            TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-08-474-040-61
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                /note= "Amino acid sequence of the heavy chain of the humanized mik-betal antibody."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.9%; Score 65; DB 1; Length 119; 78.6%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: FLORY disk
COMPUTER: IBM PC Compatible
OSPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: U-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 18-EB-1990
APPLICATION NUMBER: US 07/200,975
FILING DATE: 28-DED-1989
APPLICATION NUMBER: US 07/200,975
FILING DATE: 28-DED-1989
APPLICATION NUMBER: US 07/200,975
FILING DATE: REB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Townsend and Townsend Khourie and Crew
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPOOMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 60, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Town STREET: 39-Lytton Avenue CITY: Palo Alto STATE: California CCUNTRY: US ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                  TOPOLOGY: single TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 VIWSGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 78.61
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1.,119
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-474-040-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-474-040-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

```
; OTHER INFORMATION: heavy chain of the humanized mik-betal antibody.
US-08-487-200-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65; DB 1; Length 119;
Pred. No. 0.018;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESCEE: Townsend and Townsend and Crew STREET: 379 Lytton Avenue CITY: Palo Alto CITY: Palo Alto STATE: California COUNTRY: US ZIP: 94301 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk: COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/NMS-DOS OFTWARE: Patentin Release #1.0, Version #1. CURRENT APPLICATION NUMBER: US/08/487,200 FILING DATE: 7-UNN-1995
                                                                               DB 1;
0.018;
                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REPERENCE/DOCKET NUMBER: 11823-002610
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIPACATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-5EP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 13-FEB-1988
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                     RESULT 13
US-08-487-200-60
; Sequence 60, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
                                                                                  73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 119 amino acids
amino acid
                                                                                                                                                               1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                        50 VIWSGGSTDYNAAF 63
                                                                                  Query Match 73.9
Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-08-487-200-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
                                                                                                                                                                                                        g
                                                                                                                                                                        ò
                                                                                                                                                ö
                                                                                                         73.9%; Score 65; DB 1; Length 119; 78.6%; Pred. No. 0.018; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                             Sequence 3.2.7.3.

Sequence No. 5693762

Patent No. 5693762

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: SCHNEIDE, William P.

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Amino acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11823-002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 7 - UUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 119 amino acids
amino acid
                                                                                                                                                                                              1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                     50 VIWSGGSTDYNAAF 63
                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                         ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                         Query Match
Best Local Similarity
Matches 11; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                       d
```

```
·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                            ö
                                                                                                                                                                                                                                                                                                       APPLICANT: CO. Man Sung
APPLICANT: CO. Man Sung
APPLICANT: CO. Man Sung
APPLICANT: CO. Man Sung
APPLICANT: APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, MANDERS:
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: APPRESSE:
ADDRESSEE: 379 Lytton Avenue
Length 119
                                          Indels
```

1 VIWSGGNTDYNTPF 14

à

```
/note= "Amino acid sequence of the heavy chain of the humanized mik-betal antibody."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Sequence 37, Application US/08484537

Patent No. 6180370

GENERAL INFORMATION:
APPLICANT: OUEEN, Cary L.
APPLICANT: COLEN, Wan Sung
APPLICANT: CALNEDER, William P.
APPLICANT: CALNEDER, William P.
APPLICANT: CALNEDER, Wathleen L.
APPLICANT: CELINCH, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.9%; Score 65; DB 3; Length 119; Best Local Similarity 78.6%; Pred. No. 0.018; Matches 11; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94301

ZIP: 94301

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:

CLASSIFICATION

CLASSIFICATION

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/634,278

FILING DATE: 19-DEC-1990

FILING DATE: 28-SEP-1990

PRIOR APPLICATION NUMBER: US 07/590,274

FILING DATE: 13-FEB-1989

PRIOR APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTOMAREY/ABCHT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,233

REGISTRATION NUMBER: 30,233

REGISTRATION NUMBER: 330,233

REGISTRATION NUMBER: 330,233

REGISTRATION NUMBER: 30,233

REGISTRATION NUMBER: 30,233

REGISTRATION NUMBER: 31,223

INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 VIWSGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1.119
CTHER INFORMATION:
COTHER INFORMATION:
US-08-484-537-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                  RESULT 14
US-08-487-200-61
US-08-487-200-61
Sequence 61, Application US/08487200
Sequence 61, Application US/08487200
Sequence 61, Application US/08487200
Sequence 61, Application US/08487200
SEPPLICANT: OUEEN, Cary L.
APPLICANT: OLENGINER, William P.
APPLICANT: COELINGH, Kathleen L.
TITLE OF INVARITON: IMPROVED HUMANIZED INVANOGIOBLINS NUMBER OF SEQUENCES: 113
CORRESPONDENCES: 113
CONTRESSENDENCES: 113
CONTRESSENDENCES: 113
CONTRESSENDENCES: 113
CONTRESSENDENCES: 103
STREET: 379 Lytton Avenue
CITY: Palo Alto Ato Avenue
CITY: 105
CONTRESSENCES: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: 105
CONTRESSEN: Townsend and Townsend and Crew
MEDIUM TYPE: RIOPPY disk
OMPUTER READALD FORM:
MEDIUM TYPE: Ploppy disk
CONTRENT APPLICATION DATA: 105
CURRENT APPLICATION DATA: 105
SCTWARB: 19-DEC-190
FILING DATE: 19-DEC-190
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-DEC-190
REDICATION NUMBER: US 07/590,274
FILING DATE: 13-EB-189
RECOMMINICATION DATA: 13-EB-189
RECOMMINICATION DATA: 13-EB-189
RECOMMINICATION DATA: 13-EB-189
RECOMMINICATION NUMBER: US 07/590,975
FILING DATE: 13-EB-189
RECOMMINICATION NUMBER: US 07/590,975
FILING DATE: 13-EB-189
RECOMMINICATION NUMBER: US 07/290,975
FILING DATE: 13-ATON DATA: 05-422
FILING DATE: 13-EB-189
RECOMMINICATION NUMBER: US 07/290,975
FILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 65, DB 1, Length 119,
Pred. No. 0.018;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
                                                                                                                                            50 VIWSGGSTDYNAAF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VIWSGGNTDYNTPF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-487-200-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

Search completed: October 6, 2004, 16:36:31 Job time : 27.5789 secs

50 VIWSGGSTDYNAAF 63

RESULT 15 US-08-484-537-37

This Page Blank (uspto)

18-07-070-070-0-E

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

/ Search time 11.5789 Seconds
(without alignments)
91.382 Million cell updates/sec October 6, 2004, 16:23:59

Run on:

US-09-635-974A-6 62 1 ALTYYDYEFAY 11

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ub in	C90363	T42229 probable 1	C64483 hypothe	RRNZNV	809958	A90230 conserv	hypothetic	S35315 cell division	CEECDL	H90640 D-alanine-D-a	H85491 D-a	AG0518	T24569 hypothetical	G71853 . flagellar hoc	G64659	E72215	C97865		F90278	T17878	AC0248 hypothetica	A70107 probable g	T32099 hypothetica	A70311 hypothetica	AI0825 probable 3-ph	A83005 conserved hypothe	A45184 protein-ty	I49553	00000
		130	0	1009	N	121	130	247	299	306	306	306	306	372	909	909	642	62	119	130	249	276	335	337	348	379	428	629	629	
% Query		66.1	Ģ.		Ξ.	σ,	59.7	59.7	59.7	59.7	φ.	ď.	6	o,	59.7	59.7	59.7	œ.	8	8	58.1		58.1	ω.	58.1	58.1	58.1	58.1	ω,	
(((a core	41		40		37		37						37					36					36				36		
Result		7	7	m	4	ហ	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27		

alpha-2-macroglobu Na+-transporting A hypothetical prote B5 protein - human hypothetical prote hypothetical prote hypothetical prote hypothetical prote 3-methyl-2-oxobuta hypothetical prote hypothetical prote mypothetical prote ymothetical prote hypothetical prote hypothetical prote Typothetical prote hypothetical prote hypothetical prote hypothetical prote Typothetical prote Typothetical prote Typothetical prote	
743166 H68862 824862 WWL441 WWL441 1163453 1163454 B66655 F664736 B856496 B856496 B85699 1405599 1405599 G97272	
000000000000000000000000000000000000000	
1 4 4 4 4 4 4 4 4 4 4 4 4 4	
$\begin{array}{c} \mathbf{u} $	
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	

### ALIGNMENTS

Conserved hypothetical protein [imported] - Sulfolobus solfataricus
C.Species: Sulfolobus solfataricus
C.Species: Sulfolobus solfataricus
C.Species: Sulfolobus solfataricus
C.Species: Sulfolobus solfataricus
C.Accession: C90363
R.She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, I arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Cost, J.
A.Pbestription: Sulfolobus solfataricus complete genome.
A.Reference number: A99139
A.Accession: C90363
A.Accession: Preliminary
A.Accession: Preliminary
A.Residues: 1-130 <RUR>
A.Residues: 1-130 <RUR>
A.Residues: 1-130 <RUR>
A.Grossereferences: GB:AE006641; NID:g13815246; PIDN:AAK42162.1; GSPDB:GN00155
C.Genetics:
A.Gene: SSO1970

Gaps 0 Query Match 66.1%; Score 41; DB 2; Length 130; Best Local Similarity 70.0%; Pred. No. 4.5; Matches 7; Conservative 1; Mismatches 2; Indels

ö

|||||| :|| 89 LTYYDASYAY 98 2 LIYYDYEFAY 11 δ g

RESULT 2
742229
742229
C;Speacles: Mus musculus (house mouse)
C;Speacles: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C;Accession: T42229
R;Halleck, M.S.; Blackman, C.F.; Gao, L.; Williamson, P.L.; Schlegel, R.A.
submitted to the EMBL Data Library, June 1997
A;Description: Multiple members of a third subfamily of P-type ATPases identified by ger A;Accession: T42229
A;Accession: T42229
A;Accession: T42229
A;Accession: Multiple members of a third SPEMBL/DDBJ
A;Accession: 110209
A;Accession: T42229
A;Accession: T42229
A;Accession: T42229
A;Accession: T42229
A;Accession: T42229
A;Coss-references: EMBL:AF011336; NID:G2944186; PID:G2944187; PIDN:AAC05245.1
C;Keywords: hydrolase; transmembrane protein

Gaps . 0 Query Match
66.1%; Score 41; DB 2; Length 1020;
Best Local Similarity 87.5%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 1; Indels

ö

2 LTYYDYEF | |||||| ò

·,

Gaps

```
Conserved hypothetical protein [imported] - Sulfolobus solfataricus
CiSpecies: Sulfolobus solfataricus
CiSpecies: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
CiAccession: A02030
CiAccession: A02030
CiStory I.; Jeffries: A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragam, M.A.; Sensen, C.W.; Van der Oost, J.
Alard, Combank, April 2001
A,Description: Sulfolobus solfataricus complete genome.
A,Reference number: A99139
A,Accession: A99230
A,Accession: A99230
A,Accession: A99230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Gross-references: GB.AJ235271; GB.AJ235269; NID:g3868717; PIDN:CAA14858.1; PID:g3860956
A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein RP401 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession, H71897
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: H71697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-130 <KUR>
A;Cross-references: GB:AE006641; NID:g13813978; PIDN:AAK41096.1; GSPDB:GN00155
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-247 <AND>
A,Molecule type: mRNA
A,Residues: 1-121 <REI>
A,Cross-references: BMBL:X51846; NID:g55246; PIDN:CAA36139.1; PID:g930214
A,Cross-references: BMBL:X51846; NID:g55246; PIDN:CAA36139.1; PID:g930214
C,Superfamily: immunoglobuliu v region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.7%; Score 37; DB 2; Length 130; 60.0%; Pred. No. 22; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: RP401
C;Superfamily: Rickettsia prowazekii hypothetical protein RP401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 59.7%; Score 37; DB 2; Length 247; Local Similarity 85.7%; Pred. No. 43; es 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                      Length 121;
                                                                                                                                                                                                                         2;
                                                                                                                                                                                                        DB 7
                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                      Score 37;
Pred. No. 2
                                                                                                                                                                                                                      59.7%;
75.0%;
                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 LTYYDASYVY 98
                                                                                                                                                                                                                                                                                                                                                                                                             103 YYGYSFAY 110
                                                                                                                                                                                                                                                                                                                                                 4 YYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 YDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 зз уруштан зэ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: $500798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
                                                                                                                                                                                                                                                                                                                                                                                                                 d
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                               hypothetical protein MJ1468 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 10-Oct-1997
C;Accession: G64483
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Wosse, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: G64483
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molacule type: DNA
A;Residues: 1-1009 <BULx-A;Molacule type: DNA
A;Residues: 1-1009 <BULx-A;Molacule type: DNA
A;Cross-references: GB:UG7587; GB:L77117; NID:g1592103; PID:g1592109; TIGR:MJ1468; PID:g
C;Genetics:
A;Map position: FORL437031-1440060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 igheavy chain V-D-J region (IE10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C;Accession: S09958
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Bur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A;Reference number: S09955; MUID:90269328; PMID:2347362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome polyprotein - Newcastle disease virus (strain Beaudette C)
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: Newcastle disease virus
C;Species: Newcastle disease virus
C;Accession: A26747
R;Yusoff, K.; Millar, N.S.; Chambers, P.; Emmerson, P.T.
N;Yusoff, K.; Millar, N.S.; Chambers, P.; Emmerson, P.T.
A;Title: Nucleotide sequence analysis of the L gene of Newcastle disease virus: homologia A;Reference number: A33665; MuID:87230982; PMID:3035486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-2204 <YUS>
A;Cross-references: GB:X05399; NID:g60937; PIDN:CAA28985.1; PID:g60939
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.3%; Score 38; DB 1; Length 2204; 66.7%; Pred. No. 2.8e+02; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.5%; Score 40; DB 2; Length 1009;
85.7%; Pred. No. 56;
rative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: parainfluenza virus RNA-directed RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: L
C,Superfamily: parainfluenza virus RNA-d
C,Keywords: ATP, nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:| ||:|
TYFDSEFSY 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TYYDYEFAY 11
          LKYYDYEF 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||
TYYDYEY 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TYYDYEF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
S09958
```

₽ 임 ö

. :

ઠે g 0

Gaps

```
A; Description: catalyzes ATP-driven formation of alanyl-D-alanine from 2 alanine molecul A; Description: catalyzes ATP-driven formation of alanyl-D-alanine molecul A; Dethway: cell wall synthesis A; Mote: two D-alanine-D-alanine ligases in E. coli (and S. typhimurium) encoded by two cthe two enzymes display remarkably similar catalytic efficiencies and substrate specific C; Superfamily: D-alanine-D-alanine ligase
C; Superfamily: D-alanine-D-alanine ligase motif 1
F; 245-276 (Region: D-alanine-D-alanine ligase motif 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Delanine-D-alanine ligase B [imported] - Escherichia coli (strain O157:H7, substrain R1 C;Species: Escherichia coli (C;Species: Escherichia coli (E;Species: Escherichia coli (E;Species: Escherichia (E;Species: Escherichia (E;Species: Escherichia (E;Species: Escherichia (E;Species: Escherichia (E;Species: Escherichia coli (E;Species: Escherichia coli (E;Species: Escherichia coli (E;Species: Escherichia coli (E;Species: Escherichia (E;Species: Escherichia coli (E;Species: Escherichia (E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Accession: D64731

A;Curan-tope: DNA

A;Residues: 1-306 <a href="https://document.com/bits/">a https://document.com/bits/</a>

A;Residues: 1-306 <a href="https://document.com/bits/">a https://document.com/bits/</a>

A;Cross-references: GB;Accooll8, GB;U00096; NID:g1786262; PIDN:AAC73203.1; PID:g1786280, C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                          A, Map position: 2 min
A, Mote: gene is located in a large cluster of genes that are involved in cell division
C, Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Residues: 1-306 <HAY>
A,Cross-references: GB:BA000007; PIDN:BAB33519.1; PID:g13359552; GSPDB:GN00154
A,Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 1;
Pred. No. 54;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 2
Pred. No. 54;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: ECs0096
C;Superfamily: D-alanine-D-alanine ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                급
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TYYDYEFAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 TFYDYEAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TYYDYEFAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 TFYDYEAKY
                                                                                                                                                                                                                                                                                                                                                                                                      A, Gene: ddlB; ddl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
H85491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Reaidues: 300-306 < DEW>
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                        cell division control protein 16 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 10-Dec-1999
C;Accession: 835315; T39042
R;Fankhauser, C.; Marks, J.; Reymond, A.; Simanis, V.
A;Fankhauser, C.; Marks, J.; Reymond, A.; Simanis, V.
A;Title: The S:Dombe cdc16 gene is required both for maintenance of p34(cdc2) kinase act
A;Reference number: 835315; MJID:93327759; PMID:8334988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-306 <ROBS
A; Residues: 1-306 <ROBS
A; Coss-references: GB:X55034; NID:g40841; PIDN:CAA38869.1; PID:g40860
A; Cross-references: GB:X55034; NID:g40841; PIDN:CAA38869.1; PID:g40860
A; Experimental source: strain K-12, substrain W3110
B; Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizobu submitted to the EMBL Data Library, December 1992
A; Description: Systematic sequencing of the Escherichia coli genome: analysis of the 0-2
A; Accession: S40602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
Residues: 1-306 «YUR»
Residues: 1-306 «YUR»
Residues: 1-306 «YUR»

Dewar, S.J.; Donachie, W.D.
Bacteriol. 172, 6611-6614, 1990

Title: Regulation of expression of the ftsA cell division gene by sequences in upstrea
Reference number: A37155; MUID:91035283; PMID:2228979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -alamine-D-alamine ligase (EC 6.3.2.4) B - Escherichia coli (strain X-12)
Alternate names: alamylalamine synthetase
'Species: Escherichia coli
'Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text_change 03-Jun-2002
'Accession: A30289; A50602; 537155; D64731
'RObinson, A.C.; Kenan, D.J.; Sweeney, J.; Donachie, W.D.
'Bacteriol. 167, 809-817, 1986
'Bacteriol. 167, 809-817, 1986
'Atternor evidence for overlapping transcriptional units in an Escherichia coli
'Rocession: A30289; MUID:86304170; PMID:3528126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSPDB:GN00066; SPDB:SPAC6F6.08c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Residues: 1-29 cFANS.
A,Residues: 1-29 cFANS.
A,Cross-references: EMBL:X71605; NID:g385068; PIDN:CAA50606.1; PID:g395069
R,Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Estenties to the EMBL Data Library, September 1997
A,Reference number: Z21797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-299 <GEN>
A;Cross-references: EMBL:298981; PIDN:CAB11731.1; G:
A;Experimental source: strain 972h-; cosmid c6F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 2;
Pred. No. 52;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 1
A;Introns: 167/3; 198/1; 247/2
C;Superfamily: cell cycle arrest protein BUB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 : |: |||
212 ALTIWDFLFAY 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: S35315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \stackrel{>}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
```

g

ò

ö

Gaps

```
flagellar hook-associated protein 1 (hap1) - Helicobacter pylori (strain J99)

C;Species: Helicobacter pylori
A;Variety: strain J99
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: G71853
C;Accession: G71853
C;Accession: G71853
C;Accession: G71853
C;Accession: G71853
A;Reference number: A71800; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; JA;Reference number: A71800; MUD:99120557; PMID:9923682
A;Reference number: A71800; MUD:99120557; PMID:9923682
A;Reference number: A71800
A;Residues: Dreliminary
A;Rocession: G71853
A;Residues: 1-606 cARN>
A;Reperimental source: strain J99
C;Genetics:
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cispecies: Helicobacter pylori
Cispecies: Helicobacter pylori
Cispecies: Helicobacter pylori
Cipate: Os-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
Cipate: Os-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
Cipate: Os-Aug-1997 #sequence D: Dodson, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.
Nature 388, 539-547, 1997
Nature 388, 539-547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: GB:AE000618; GB:AE000511; NID:g2314268; PIDN:AAD08163.1; PID:g2314277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             flagellar hook-associated protein 1 - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 2; Length 606
Pred. No. 1.1e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 2; I
Pred. No. 1.1e+02;
2; Mismatches 1;
     Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: October 6, 2004, 16:34:50 Job time : 15.5789 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.7%;
     ilarity 55.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                         |:|:||:|
41 AMTHYDFDF 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||| ||:
86 TYYDTEFSH 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||| ||:
86 TYYDTEFSH 94
                                                                                                                                                             σ
                                                                                                                                                             1 ALTYYDYEF
     Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-606 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues:
                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
AG0518
D-alanine, D-alanine ligase B [imported] - Salmonella enterica subsp. enterica serovar Typhi
C.Species: Salmonella enterica subsp. enterica serovar Typhi
G.Species: Salmonella enterica subsp. enterica serovar Typhi
A,Note: this species has also been called Salmonella typhi
C.Species: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C.Accession: AG0518
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Daviss, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
A; Mulle, S.; O'Gaora, P.
A; Mulle Gomplete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; MUDD:21534947; PMID:11677608
A; Actuals preliminary
A; Cross-references: GB:AL513382; PIDN:CAD01287.1; PID:g16501415; GSPDB:GN00176
C; Genetics:
A; Ge
A;Accession: H85491
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-306 <STO>
A;Cross-references: GB:AE005174; NID:g12512798; PIDN:AAG54396.1; GSPDB:GN00145; UWGP:Z01
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Genee: ddlB
C;Superfamily: D-alanine-D-alanine ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T24569
T24569
hypothetical protein T06C12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 20-Jun-2000
C;Accession: T24569
R;Kelly, P. submitted to the EMBL Data Library, October 1996
A;Reference number: 219908
A;Reference number: 219908
A;Reference number: 219908
A;Reference number: 219908
A;Recession: T24569
A;Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: CBSP:T06C12.4
A,Map postition: A,A,Introns: 66/2; 290/3
C,Superfamily: Caenorhabditis elegans hypothetical protein C36C9.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 2; Length 306;
Pred. No. 54;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 306; 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.7%; Score 37; DB 2; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.7%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 TFYDYEAKY 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 TFYDYEAKY 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
```

g

ö

Gaps

. 0

ö

Gaps

; 0

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

October 6, 2004, 16:21:13 ; Search time 6.75439 Seconds (without alignments) 84.800 Million cell updates/sec Run on:

US-09-635-974A-6 62 1 ALTYYDYEPAY 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% ... Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description			mernanococ	newcast					escherichi				075110 homo sapien	mus	P46795 borrelia bu	066516 aquifex aeo		HOH	P35991 mus musculu	bac	P27227 human papil	Q8eyp6 leptospira	Q8zrr0 salmonella	Q8x929 escherichia	ø	escheric		P54528 bacillus su		75 mycopl	34	schizo	P49753 homo sapien	12 saccha
OH INGHIO	Ð	Catter cate	- 1	- 1	KKPL NUVB	Y401_RICPR	CC16 SCHPO	DDLB_ECO57	DDLB_ECOL6	DDLB_ECOLI	DDLB_SALTI	DDLB_SALTY	DDLB SHIFL	AT9A_HUMAN	AT9A MOUSE	G3P_BORBU	Y113_AQUAE	HGD_LEGPN	BIK_HUMAN	BIK_MOUSE	PCRA_BACST			PANB_SALTY		PANB_ECOL6		PANB_SALTI		DDLB_CHRVO	Y308_MYCGA	LUM_HUMAN	GTP1_SCHPO		VAN1_YEAST
	03	-	4 -	4 +	4	н	н										-	н			H	-	-	Н	Н	н	-	Н	н	н	-1	-	Н	러.	m
	Query Match Length	2.5	) (	) C	?	4.	on.	$\circ$	0	0	0	0	30	1047	04	m	4	Н.	Ŋ	629	S	g)	ø	9	9	9	9	Q	0	0	0	m	364	N	ന
æ	Query Match	A 03	· <	r -		59.7	σ,	о О	σ.	თ	ი	59.7	ა	σ.	σ.	œ.	œ.	œ.	œ.	m	m	· ·	'n	'n.			'n						56.5		
	Score	43	} <	יי פיי	91	3.7	37	37	37	37	37	37	37	37	37	36	36	36	36	36	36	32	35	35	35	35	32	32	32	32	32	32	e B	32	35
	Result No.	-	10	1 (	η.	4.	ເດ	vo	7	ш	σ'n	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	26	27	28	20	30	31	32	33

P09303 varicella-z P35830 thermus the C53226 rhodobacter Q04768 lactcoccus Q04774 lactcoccus Q98005 sulfolobus Q9526 lactcoccus Q9529 neisseria m Q96000 neisseria m P51640 mesocricetu Q91676 pseudomonas	
HELI _VZVD SLAP_THETH PYP_RHOSH PYO34_BPLLH YG34_BPLLH YG34_BPLLH YS56_SULSO YSDJ_LACLA DDL_NEIMA DDL_NEIMA DDL_NEIMB DDL_NEIMB BOLL NEIMB G3P_MESAU	
ппппппппппппппппппппппппппппппппппппппп	
N N N N N N N N N N N N N N N N N N N	
N N 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩	

# ALIGNMENTS

RESULT 1

OCOUNTY OF THE PROPERTY OF THE	CANDO CKR3 CANDO CKR3 CANDO (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence 10-OCT-2003 (Rel. 39, Last sequence 10-OCT-2003 (Rel. 39, Last sequence 10-OCT-2003 (Rel. 39, Last sequence CCR3 ON CKRBR3. CCR3 ON CCR3 ON CR3 ON CCR3 ON CR3 ON CCR3 ON CR3 ON CCR3 ON CR3	STANDARD; PRT; 358 AA.	Rel. 39, Created) Rel. 39, Last sequence update) Rel. 42, Last annotation update) receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3)	(CCR3 OR CMKBR3. Cavia porcellus (Guinea pig). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Hystricognathi, Caviidae, Cavia. NCBL_TaxID=10141;	[1] SEQUENCE FROM N.A. MEDINE-99049845; PubMed-9834099; Sabroe I., Conroy D.M., Gerard N.P., Li Y., Collins P.D., Post T.W., Jose P.J., Williams T.J., Gerard C.J., Ponath P.D.; "Cloning and characterization of the guinea pig eosinophil eotaxin "Cloning and characterization of the Pulmea pig eosinophil eotaxin "Receptor, C-C chemokine receptor-3: blockade using a moncolonal	be chemokine. Binds to ectaxin, sequently transduces a signal by clum ions level (By similarity). The sembrane protein.	try is copyright. It is productions that it is productions as long as it institutions as long as it statement is not removed. Usa a license agreement (See http: olicense@isb-sib.ch).	C80428.1; 6; GPCR_Rhodpsn. 1; 1. 1. PCRRHODOPSN. PCRRHODOPSN. G PROTEIN RECEP F1 1; 1. G_PROTEIN_RECEP_F1_2; 1.	
	CAVPO CCR23 30-MAY-2000 30-MAY-2000 10-OCT-2000 10-OCT-2000 CCC chemok. CCC ch	STAN	) (Rel. 3) (Rel. 3) (Rel. 4) (Rel. 4) (Ine recept	CBR3. ellus (Gu Metazoa; Sutheria;	COM N.A. Conroy D Williams Charac	1 vivo."; 161:613 N: Recep MCP-4 an Ming the ULAR LOC	PROT ent swiss in Bioinf nn-profit du this s	100698; AAC 100001; 7tm 10001; 7tm PR00237; GP PS00237; GP PS50262; G	

Gaps

..

Indels

. 0

```
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
Y401 RICPR STANDARD; PR:
1D Y401 RICPR STANDARD; PR:
AC Q9ZDD0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 39, Last sequen
DT Hypothetical protein RP401.
  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X05399; CAA28985.1; -.
  6; Conservative
                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       878 TYFDSEFSY 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TYYDYEFAY 11
                                                                                      399 TYYDYEY 405
                                          3 TYYDYEF 9
                                                                                                                                                       RESULT 3
RRPL NDVB
ID RRPL NDVB
  Matches
                                                                                                                                                                                                                        SAN DEPARTMENT OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       유
                                                                                      g
                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=96337999; PubMed=868887;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstoock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weinstoock K.G., Merrick J.M., Glodek A.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 273:1058-1073(1996).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Contains 5 PKD domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; MJ1468; -.
InterPro; IRPG00601; PKD.
Pfam; PF00801; PKD; 5.
SWART; SM00089; PKD; 7.
PROSITE; PS50093; PKD; 5.
Hypotherical protein; Transmembrane; Repeat; Complete proteome.
TRANSMEM 6 26 POTENTIAL.
TRANSMEM 6 26 POTENTIAL.
                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 1; Length 1009; Pred. No. 31;
                                                                                                             Score 43; DB 1; Length 358; Pred. No. 3.4; 0; Indels 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW; 13E9B4933EAB7972 CRC64;
                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
7B73FAB7A3BC3670 CRC64;
  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea, Buryarchaeota, Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein MJ1468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-ASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKO 3.
PKO 4.
                                                                        41623 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U67588; AAB99478.1; -. PIR; C64483; C64483.
                                                                                                                    69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115119
                                                                                                                                       87.5%;
                                                                                                                                       Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanococcus jannaschii
    287
308
358
                                                                                                                                                                                                        3 TYYDYEFA 10
                                                                                                                                                                                                                                                  TFYDYEFA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1009 AA;
                                                                        358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR, MJ1468;
InterPro; IPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annaschii.
                                                                                                                                                                                                                                                                                                                                                              METJA
      DOMAIN
TRANSMEM
                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                              058863;
                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MJ1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                임
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bainformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                         01-0TL-1989 (Rel. 11, Created)
01-UTL-1989 (Rel. 11, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
RARA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
(L protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=8730982; PubMed=3035486; Emmerson P.T.; Milar N.S., Chambers P., Emmerson P.T.; Vusial 200982; PubMed=3035486; Milar N.S., Chambers P., Emmerson P.T.; Milar N.S., Chambers P., Sendal and Vesicular stomatitis viruses."; Nucleic Acids Res. 15:396(1-397).

-I. FUNCTION: Probable component of the active polymerase. It may function in mRNA synthesis, capping, methylation and poly(A) synthesis of newly synthesis of newly synthesized viral mRNAs, RNA editing of the Pendent transcript, and protein kinase activity.

-I. ÇATALITIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the paramyxoviruses L protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Length 2204; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                  L. Newcastle disease virus (strain Beaudette C/45) (NDV). Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Rubulavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007098; RNA_pol_monon.
InterPro; IPR001016; Viral_RNA_pol_L.
Pfam; PF00946; Paramyx_RNA_pol_1.
Transferase; RNA-directed RNA_polymerase.
SEQUENCE 2204 AA; 248822 MW; C67B8674D904802C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 AA.
2204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COSCIENTAR
```

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDLB ECC57
AC 08X9Ke,
DT 28-FEB-2003
DT 28-FEB-2003
DT 28-FEB-2003
DT 10-CT-2003
DE D-alanine-DE Synthetase B GN DDLB OR Z010
CS Bacteria; Proce CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobacter
CC Enterobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell cycle.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-2164401; PubMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

Holroyd S., Hornsby T., Howarth S., Hockle E.J., Hunt S., Jagels K.,

James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

Oliver K., O'nell S., Pearson D., Quall M.A., Rabbinowitsch E.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE 99327759; PubMed=8334988; Fankhauser C., Marks J., Reymond A., Simanis V.; Fankhauser C. Marks J., Reymond A., Simanis V.; The S. pombe cdc16 gene is required both for maintenance of p34cdc2 kinase activity and regulation of septum formation: a link between mitosis and cytckinesis?; EMBO J. 12:2697-2704(1993).
                                                                                                                Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.7%; Score 37; DB 1; Length 247; 85.7%; Pred. No. 25; 1. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ235271; CAA14858.1; -.
PIR; H1687; H71697.
HYPOChbet.cal protein; Complete proteome.
SEQUENCE: 247 AA; 28125 MW; A30702F1912543D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Pungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CDC16 OR SPAC6F6.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 AA
                                                                      STRAIN=Madrid E;
MEDLINE=99039499; PubMed=9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85...,
6; Conservative
                                                                                                                                                                                                                                      Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 YDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDYEFAH 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
  NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHPO
ð
```

```
Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehzach H., Reinhardt R., Pohl T.M., Berzym K., Langer I., Beck A., Lehzach H., Reinhardt R., Pohl T.M., A Gefeu A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galbert F., Aves S.J., Xiang Z., Hunt C., More K., Hurst S., Mottier S., Dominguez A., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Amastrong J., Forsburg S.L., A Dominguez A., Revuelta J.L., Moreno S., Amastrong J., Forsburg S.L., Rature 415.871-880(2002).

A Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., The genome sequence of Schizosaccharomyces pombe.";

Nature 415.871-880(2002).

INVOLVED IN MAINTENANCE OF CDCZ KINASE ACTIVITY. IT IS
SUBSEQUENTLY REQUIRED FOR REGULATION OF SEFTUM FORMATION.

C. INVOLVED IN MAINTENANCE OF CDCZ KINASE ACTIVITY BY PREVENTING, DIRECTLY OR INDIRECTLY, THE DESTADATION OF CYCLIN OR THE DEHOSPHORYLANION OF THR. 167 OF CDCZ.

C. INVALVE SIMILARITY: Contains 1 Rab-GAP TBC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
10-Alamine-D-alamine ligase B (EC 6.3.2.4) (D-alamylalanine synthetase B) (D-Ala-D-Ala ligase B).
10-BDB OR ES0096.
10-Botherichia coli 0157.H7.

Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.7%; Score 37; DB 1; Length 299; 63.6%; Pred. No. 30; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 299 AA; 33988 MW; 8958846E4032766D CRC64;
Robben J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAB-GAP IBC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenedB SPombe; SPAC6F6.08c; -.
InterPro; IPR000195; RabGAP_TBC.
Pfam; PF00566; TBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50086; TBC_RABGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X71605; CAAS0606.1; -.
EMBL; Z98981; CAB11731.1; -.
PIR; S35315; S35315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| :|: |||
212 ALTIWDFLFAY 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00164; TBC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 7; Conserv
```

```
Ouery Match
Best Local Similarity 60...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|||| |
207 TFYDYEAKY 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149
189
280
305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
DDLB ECOLI
ID DDLB ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P07862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID DOT SERVING CONTRACTOR SERVIN
SOUTH THE TENT OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBBUTT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-CCT-2003 (Rel. 42, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.7%; Score 37; DB 1; Length 305; 66.7%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B8C61308C79F36F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ligase, Cell wall, PeptidogTycan synthesis, INIT MET 0 0 BY SIMILARITY. ACT SITE 14 14 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00047; -; 1.

InterPro; IPR00505; D ala D ala.

InterPro; IPR000291; Dala Ligas; 1.

Pfam; PF01820; Dala Dala Ligas; 1.

Pfam; PF01820; Dala Dala Ligas; 1.

PROSTIE; PS00843; DALA DALA LIGASE 1: 1.

PROSTIE; PS00844; DALA DALA LIGASE 2: 1.
                                                                                                                                                                                             [2]
STRAIN=CLS7:H7 / RIMD 0509952;
STRAIN=CLS7:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AE005186; AAG54396.1; -. BMBL, AP002550; BAB33519.1; -. PIR, H85491. H85491. PIR, H90640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32722 MW;
                                                                                                       "Genome sequence of enter
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149
280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 TFYDYEAKY 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alanyl-D-alanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
149 1
280 2
305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDLB ECOL6
Q8FL63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
DDLB_ECOL6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRARE REPARE REP
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
              Gaps
                                                                                                                                                                                                                                                                                  alanyl-D-alanine.
-!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second
                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robinson A.C., Kenan D.J., Sweeney J., Donachie W.D.; "Further evidence for overlapping transcriptional units in an Escherichia coli cell envelope-cell division gene cluster: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1988 (Rel. 08, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-CCT-2003 (Rel. 25, Last annotation update)
D-alanine-D-alanine ligase B (EC 6.3.2.4) (D-alanylalanine synthetase B) (D-Ala-D-Ala ligase B).
DDLS OR DDL OR B0092.
Escherichia coll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 1; Length 305;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E09D9604F7D5BF0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXBL; ABO16755; rem.

HAWAP; MF 00047; -; 1

R InterPro; IPR002091; Dala lig Van.

R PGam; PF01820; Dala Dala ligas; 1

R TGRFAM; TGR01205; Dala Dala Ligas; 1

R PROSITE; PS00843; DALA DALA LIGASE 1; 1

DR PROSITE; PS00844; DALA DALA LIGASE 2; 1

ET INIT MET 0 0 0 BY SIMILARITY.

FT ACT SITE 14 14 BY SIMILARITY.

FT ACT SITE 149 149 BY SIMILARITY.

FT ACT SITE 149 149 BY SIMILARITY.

FT ACT SITE 149 149 BY SIMILARITY.

FT ACT SITE 149 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
MEDLINE=22388234; PubMed=12471157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12;
MEDLINE=86304170; PubMed=3528126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.7%;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              Ikeda M., Wachi M., Jung H.K., Ishino F., Matsuhashi M.;
"Nucleotide sequence involving murG and murC in the mra gene cluster
region of Escherichia coll.";
Nucleic Acids Res. 18:4014-4014(1990).
                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-KIZ / MG1655;
STRAIN-KIZ / MG1655;
BLATINE-97426617; PubMed=9278503;
BLATINE-97426617; PubMed = 9.278503;
BLATINE-P.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y., "The complete genome sequence of Escherichia coli K-12.";
science 277:1453-1474(1997).
 sequence and transcriptional organization of the ddl ftsQ region."; J. Bacteriol. 167:809-817(1986).
                                                                                         Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.; "Systematic sequencing of the Escherichia coli genome: analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-95025539; PubMed=7939684;
Fan C., Moews P.C., Walsh C.T., Knox J.R.;
"Vancomycin resistance: structure of D-alanine:D-alanine ligase at 2.3-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBGNIT: Monomer.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-XAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=97207065; PubMed=9054558;
Fan C., Park I.-S., Walsh C.T., Knox J.R.;
Fan C., Park II.-S., Walsh C.T., Knox J.R.;
"D-alanine:D-alanine ligase: phosphonate and phosphinate
intermediates with wild type and the Y216F mutant.";
Biochemistry 36:2531-2538(1997).
-! FUNCTION: Cell wall formation.
-! CATALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate + D-alanyl-D-alanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92207163; PubMed=1554356; Albar O.A., O'Connor C.D., Giles I.G., Akhtar M.; "D-alanine-D-alanine ligase of Escherichia coli. Expression, purification and inhibitory studies on the cloned enzyme."; Biochem. J. 282:747-752(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION, AND PARTIAL SEQUENCE.
                                                                                                                                       the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
                                                                            MEDLINE=92334977; PubMed=1630901;
                                                                                                                                                                                                                                                                                                                                                                              TEDLINE=90326550; PubMed=2197603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M14029; AAA23672.1; -.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-40 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 266:439-443(1994).
                                           SEQUENCE FROM N.A.
```

```
Gaps
                                                                                                                                                                                                      .
0
Score 37; DB 1; Length 305;
Pred. No. 31;
1; Mismatches 2; Indels
                                                                                                                                                                                          32708 MW; 79103A85E732A4C7 CRC64;
                                                                                                                                                                                               59.7%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                           3 TYYDYEFAY 11
                                                                                                                                                                                          305 AA;
                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                      9
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                           à
```

X55034; CAA38869.1; -. D10483; BAB96660.1; -. AE000118; AAC73203.1; CAA36869.1; -

EMBL; EMBL; EMBL;

X52644;

Gaps

ö

Indels

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 AA;
                                                                                                                                                                                                                                                                   28-FEB-2003
.
9
                                                                                                                                                                                                                  DDLB_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
  Matches
                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      유
                                                à
                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-BROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMedt G. II., Mayhew G.F., Rose D.J.,
Deng W., Liou S.-R., Plunkett G. II., Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Bakham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CIT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.
                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: Cell wall formation (By similarity).
-!- CATALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate + D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL627265; CAD01287.1; --
EMBL; AE016834; AA067866.1; --
HAMAP; ME_00047; --; 1.
InterPro; IPR005991; Dala Dala.
InterPro; IPR00291; Dala Diala ligava.
PEfam; PE01820; Dala Dala ligasi.
TIGRPAMS; TIGR01205; Dala DalaTigasi.
PROSITE; PS00843; DALA_DALA_LIGASE_1; 1.
PROSITE; PS00844; DALA_DALA_LIGASE_1; 1.
Ligase; Cell wall; Peptidoglycan synthesis; Complete proteome.
INIT_MET
                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-Cor-2003 (Rel. 42, Last annotation update)
10-dalanine-D-alanine ligase B (EC 6.3.2.4) (D-alanylalanine synthetase B) (D-Ala-D-Ala ligase B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.7%; Score 37; DB 1; Length 305; 66.7%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFD64EADC90FF003 CRC64;
                                                                                                                             305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Salmonella
NCBL_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32519 MW;
                                                                                                                                STANDARD;
          207 TFYDYEAKY 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alanyl-D-alanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              Salmonella typhi
                                                                                                                             DDLB SALTI
0829G7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                SS TWANT BEAR TO THE STANT OF T
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.

STRAIN-LTZ / SGSC1412 / ATCC 700720;

STRAIN-LTZ / SGSC1412 / ATCC 700720;

MEDLINB-21534948; PubMed=11677609;

MCClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - !- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBUNIT: MOLOGATION: Cytoplasmic (By similarity).
-!- SUMILARITY: Belongs to the D-alanine--D-alanine ligase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:852-856(2001).
-!- FUNCTION: Cell wall formation (By similarity).
-!- CATALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate + D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP: MF 00047; -; 1.
InterPro; IPR005905 Dala Dala.
InterPro; IPR005905 Dala Dala Dala.
Pfam; PF01820; Dala Dala ligas; 1.
TIGRRAMS; TIGR01205; D. ala DalaTIGR; 1.
PROSITE; PS00843; DALA DALA LIGASE 1; 1.
PROSITE; PS00844; DALA DALA LIGASE 1; 1.
Ligase; Cell wall; Peptidoglyan synthesis; Complete proteome.
INIT MET 0 0 By SMILARITY.
                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
D-alanine--D-alanine ligase B (EC 6.3.2.4) (D-alanylalanine synthetase B) (D-Ala-D-Ala ligase B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259D3960024BB700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 1;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE008700; AAL19094.1; -. Stydene; SG????; ddlB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32504 MW;
                                                                                                                                                                                                                                                                                            (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 66.7
les 6; Conservative
                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDLB OR STM0130.
Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 TFYDYEAKY 215
                                                             207 TFYDYBAKY 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alanyl-D-alanine.
3 TYYDYEFAY 11
```

RESULT 11

Euteleostomi;

Homo sapiens (Himan). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

SEQUENCE OF 15-1047 FROM N.A. (ISOFORM SHORT)

NCBI_TaxID=9606;

AT9A HUMAN STANDARD; PRT; 1047 AA. 075110; Q9NOK6; Q9NOK6; QSOX7110; QSOONC6; QSOX7110; QSOCOK6; QSOX7110; QSOCOK6; QSOX7110; QSOX712001 (Rel. 40, Last sequence update) 10-0CT-2001 (Rel. 42, Last annotation update) Potential phospholipid-transporting ATPase IIA (EC 3.6.1.-). ATP9A OR KIAA0611.

DDLB SHIFL

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=301 / Serotype 2a,
MEDLINE=22272406; PubMed=12384590;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin O., Yuan E., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=2457T / ATC. 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
Wel J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Wel J., Goldberg M.B., Parland V., Venkatesan M.M., Darling M.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";
Infect. Immun. 71275-2786(2003)
-!- FUNCTION: Cell wall formation (By similarity).
-!- CATALITIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate + D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF 00047; -1.

InterPro; IPR00291; Dala lig Van.

InterPro; IPR005905; Dala Dala Dala.

Pfam; PF001820; Dala Dala Jala.

IGRPAMS; TIGR01205; Dala DalaTIGR; 1.

PROSITE; PS00843; DALA DALA LIGASE 1; 1.

PROSITE; PS00844; DALA DALA LIGASE 2; 1.

Ligase; Cell wall; Peptidoglycan synthesis; Complete proteome.

CONFLICT 65 R -> P (IN REF. 2).
                                     Q83NF7; Q70DS4; C70DS4; C70DS5; C70DS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 AA; 32821 MW; A07A81804D4AADB6 CRC64;
          306 AA
          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE015047; AAN41754.1; -. EMBL; AE016978; AAP15635.1; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alanyl-D-alanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=301 / Serot)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              Shigella flexner
     SHIFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                           SO TENT TO THE TOTAL TO THE TOTAL TO THE TRANSPORT OF THE
```

```
RN SEQUENCE FROM N.A. (ISOPCRMS LONG AND SHORT).

RN SEQUENCE FROM N.A. (ISOPCRMS LONG AND SHORT).

RA Deloukas P., Matthews L.H., Abalurst J., Babbage A.K., Bagguley C.L.,

RA Deloukas P., Matthews L.H., Abalurst J. B., Beare D.M.,

RA Bailey O.P., Barle C.P., Blakes K.N., Beard L.M., Beare D.M.,

RA Bailey O.P., Bird C.P., Blakes K.N., Carder C., Carter N.P.,

RA Chapman J.C., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Chapman J.C., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Clegg S., Cobley V.B., Collier R.E., Comnor R.E., Corby N.R.,

RA Clison A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Ellington A., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Huckle E., Hunt A.R., Hunt S.B., Jekosch K., Johnson C.M., Johnson D.,

RA Huckle E., Hunt A.R., Hunt S.B., Jekosch K., Johnson D.,

RA Minne S.A., Mistry D., Moconmachie L.J., Notay R.N., Minkurray A.A.,

RA Minne S.A., Mistry D., Mocore M.J.F., Mullikin J.C., Nickerson T.,

RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,

RA Tracey A., Tromans A.C., Vaudin M., Walli M., Wallis J.M.,

RA Tracey A., Tromans A.C., Vaudin M., Wallis J.M.,

RA Mintehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Williming D., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RA Rogers J.,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=075110-2; Sequence=VSP_000412;
SIMILARITY: Belongs to the cation transport ATPases family (P-type
ATPases). Subfamily IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).
-!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-!- SUBCELUTAR LOCATION: Integral membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
MEDLINE=98403880; PubMed=9734811;
Ishikawa K., I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Ishikawa K., Nomura N., Ohara O.,
"Prediction of the coding sequences of unidentified human genes. X.
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Long;
IsoId=075110-1; Sequence=Displayed;
```

, 1s₁

ô

Gaps

.. 0

Indels

Pred. No. 31; 1; Mismatches

59.7%; Score 37; 66.7%; Pred. No.

Query Match
Best Local Similarity 66.7
Matches 6; Conservative

216

208 TFYDYEAKY

3 TYYDYEFAY 11

ò g

DB 1; Length 306;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIŜSUB-Brain;
MEDLINE-2047314; PubMed-11015572;
Halleck M.S., Lawler J.F. Jr., Blackshaw S., Gao L., Nagarajan P.,
Hacker C., Pyle S., Newman J.T., Nakanishi Y., Ando H., Weinstock D.,
Williamson P., Schlegel R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                       Genew, HGNC:1340; ATP84.

Genew, HGNC:1340; ATP84.

InterPro; IPR00157; ATP84e_E1-E2.

InterPro; IPR005839; Plippase.

InterPro; IPR005834; Hydrolase.

Pfam; PF00702; Hydrolase; 1.

Pfam; PF00702; Hydrolase; 1.

TIGREAMS; TIGR01652; ATP84e-Plipid; 1.

TIGREAMS; TIGR01652; ATP84E-Plipid; 1.

Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding; Alternative splicing; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MISSING (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AT9A_MOUSE STANDARD; PRT; 1047 AA.
070228; Q8VDIS; Q922L9;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Potential phospholipid-transporting ATPase IIA (EC 3.6.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1; Length 1047; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW; 80C307CF5A396755 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                             EMBL, AL138807; CAB92773.1; -.
EMBL, AL035684; CAB63450.1; -.
EMBL, AL138807; CAB92774.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1047 AA; 118582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 75.0
es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                006
030
047
391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           738 LKYYEYEF 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LTYYDYEF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
STATE THE FETTING STATES THE STATES TO SERVICE STATES THE STATES T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE STATE OF THE S
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                  SEQUENCE FROM N.A.

**REDLINE=2238857; PubMed=12477932;

**REDLINE=2238857; PubMed=12477932;

**REDLINE=2238857; PubMed=12477932;

**REDLINE=2238857; PubMed=12477932;

**REDLINE=2238857; PubMed=12477932;

**REDLINE=2238857; PubMed=12477932;

**REDLINE=228857; PubMed=1287; PubMed=127;

**REDLINE=228857; PubMed=1287; PubMed=127; PubMed=127;

**REDLINE=228857; PubMed=127; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 28-1047 FROM N.A.
MEDLINE-98217376; PubMed-9548971;
Halleck M.S., Pradhan D., Blackman C.F., Berkes C., Williamson P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphorylation; Magnesium; ATP-binding;
Differential expression of putative transbilayer amphipath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF00702; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
TIGRRAMS; TIGR01652; ATPASE-Plipid; 1.
TIGRPAMS; TIGR01494; ATPASE_P-type; 7.
PROSITE; PS001164; ATPASE E1 E2; 1.
Hydrolase; Transmembrane; Phosphorylati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF152243; AAF08396.1; -.
EMBL; BC021336; AAC05245.1; -.
EMBL; BC00621814; AAAF21814.1; -.
EMBL; BC00651819; AAH6549.1; -.
PIR; T42229; T42229.
MGD; MGI:1330826; AEP9a.
InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR005639; Flippase.
InterPro; IPR005834; Hydrolase.
                                                                   Physiol. Genomics 1:139-150(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
91
93
93
93
93
93
93
94
95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlegel R.A.;
                                            transporters.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
           THEFFE IN THE SHARE BEARE BEAR
```

```
DR EMBL; U28760; AAB53930.1; -.

DR EMBL; D28760; AAB53930.1; -.

DR EMBL; A2001119; AAC66450.1; -.

DR HIS, A70107; A70107.

DR HSSP; P00362; 1GD1.

DR HSSP; P00362; 1GD1.

DR INTERPO; IPR006424; GAPDH-I.

DR INTERPO; IPR006424; GAPDH-I.

DR FAUN; PR02007; GAPDH C: 1.

DR PINTS; PR00078; G3PDHDRGNASE.

DR PRINTS; PR00078; G3PDHDRGNASE.

DR PRINTS; PR000718; GAPDH-I; 1.

DR PROSITE; PS00071; GAPDH-I; 1.

RW Glycolysis; Oxidoreductase; NAD; Complete proteome.

FT BINDING 153 153 GALCARALDENTOR 3-PHOSPHATE.

ATT SITE 180 ATTLVATES THOLD GROUP DURING CATALVSIS.

A-> P (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.B., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                 + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                     Nature 390:580-586 (1997).

-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + pho
-!- NAD (+) = 3-phospho-D-glyceroyl phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- SUBGINIT: Homotetramer (By similarity).
-!- SUBGINIT: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.1%; Score 36; DB 1; Length 335; 60.0%; Pred. No. 50; tive 2; Mismatches 2; Indels
   Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bācteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 294 A -> P (IN REF. 1).
4 294 S -> P (IN REF. 1).
AA, 36254 MW, 30E94F988339819C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AQ_113 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=VF5; MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last seq
16-0CT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 LSWYDNEFGY 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ_113.
Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y113 AQUAE
066516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT SITE
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y113_AQUAE
REPERT OF THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANGE OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAINS—ATCC 35210 / B31;
STRAINS—ATCC 35210 / B31;
STRAINS—ATCC 35210 / B31;
BY EXAMS—ATCC 35210 / B31;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-P., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterbook T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBL_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G3P_BORBU STANDARD; PRT; 335 AA.
P467935; O510B4;
01-NOV-1995 (Rel. 32, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
G1yceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
GAP OR BBOG57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
R -> K (IN REF. 3).
V -> I (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 1; Length 104
Pred. No. 1.1e+02;
1; Mismatches 1; Indels
                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                               POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                               999
1006
1030
1047
391
785
785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        738 LKYYEYEF 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      784 78
1047 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LIYYDYEF
                                                        DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
MOD_RES
METAL
                                                                                                                                                   TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G3P BORBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
```

원 ð

ö

```
CC use by non-profit institutions as long as its content is in no way conditied and this statement is not removed. Usage by and for commercial contines requires alicenseal agreement (See http://www.isb-sib.ch/announce/CC or send an enail to licenseal sb.ch).

DR EMBL; AE000674; AAC06480.1; ...

DR PIR; A70311; A70311.

KW Hypothetical protein; Signal; Complete proteome.

FT SIGNAL 18 348 Hypothetical protein; Signal; Complete proteome.

FT CHAIN 18 348 Hypothetical protein; Signal; Complete proteome.

FT CHAIN 18 348 Hypothetical protein; Signal; Complete proteome.

FT CHAIN 18 348 Hypothetical protein; Signal; Complete proteome.

FT CHAIN 18 348 Hypothetical protein; Signal; Complete proteome.

FT CHAIN 18 348 Hypothetical protein; Signal; Complete proteome.

FT CHAIN 18 348 Hypothetical protein; Signal; Complete proteome.

FT CHAIN 18 348 Hypothetical protein; Signal; Complete proteome.

Ouery Match 58 1%; Score 36; DB 1; Length 348; Best Local Similarity 85.7%; pred. No. 52; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Indels 0; Signal; ```

Search completed: October 6, 2004, 16:30:25 Job time: 7.75439 secs

```
October 6, 2004, 16:23:13 ; Search time 36.8596 Seconds (without alignments) 94.160 Million cell updates/sec
                                                                                                                                                                                                                             1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                    1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                US-09-635-974A-6
62
1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                Title:
Perfect score:
Sequence:
                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                    Searched:
                                                                    Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |      | 110000                   | nescribtion                             | Q8i3q3 plasmodium | Q8p041 streptococc | Q8k6n0 streptococc | Q97wy9 sulfolobus | Q8e3el streptococc | Q8dxs1 streptococc | Q860w8 mus musculu | O85zw9 mus musculu | Q857e5 mycobacteri | Q9cv82 musculu | Q89y18 bacteroides | Q9emu7 amsacta moo | Q8xle4 clostridium | Q8p7x5 xanthomonas | 08jqw5 rana ridibu | Q8sqj3 encephalito |
|-----------|------|--------------------------|-----------------------------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES |      | £                        | 1                                       | 081303            | Q8P041             | OBKENO             | Q97WY9            | Q8E3E1             | Q8DXS1             | Q860W8             | Q85ZW9             | Q857E5             | Q9CV82         | QB9YL8             | Q9EMU7             | Q8XLE4             | Q8P7X5             | Q8JGW5             | Q8SQJ3             |
|           |      | Juery<br>Match Length De | and make                                | 2054 5            | 259 16             | 259 16             | 130 17            | 210 16             | 210 16             | 323 7              | 329 7              | 77 9               | 495 11         | 580 16             | 148 12             | 154 16             | 255 16             | 333 13             | 465 5              |
|           | de ( | Query<br>Match 10        | יייייייייייייייייייייייייייייייייייייי  | 71.0              | 69.4               | 69.4               | 66.1              | 66.1               | 66.1               | 64.5               | 64.5               | 62.9               | 62.9           | 62.9               | 61.3               | 61.3               | 61.3               | 61.3               | 61.3               |
|           |      | 9                        | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 44                | 43                 | 43                 | 41                | 41                 | 41                 | 40                 | 40                 | 39                 | 39             | 39                 | 38                 | 38                 | 38                 | 38                 | 33                 |
|           |      | Kesutt                   |                                         | -                 | 7                  | e                  | 4                 | Ŋ                  | ø                  | 7                  | 80                 | σ                  | 10             | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 |

| 093wc0 hordeum vul<br>089q19 bradyrhizob<br>087jtl vibrio para<br>Q8nb73 homo sapien<br>094836 homo sapien | 8 garl<br>1 garl<br>1 garl<br>8 huma | O99xa7 human immun<br>O99xa6 human immun<br>O9uxi4 sulfolobus<br>O8zuj3 pyrobaculum |                                                                                                                                                                                                                                  |                                                                                         | 09sk94 helicobacte<br>02s744 helicobacte<br>Q8s81 bacteriopha<br>Q9x868 thermotoga<br>Q88es2 pseudomonas |
|------------------------------------------------------------------------------------------------------------|--------------------------------------|-------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------|
| 503 10 Q93WC0<br>547 16 Q89QL9<br>721 16 Q87JT1<br>16 4 Q9NB73<br>1096 4 Q94836                            | 12<br>12<br>12<br>15                 | 24 15<br>26 15<br>30 17                                                             | 81 12 666 2 6 60 16 60 16 60 16 93 16 93 16 93 16                                                                                                                                                                                | 333<br>34<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13 |                                                                                                          |
| 38 611.3<br>38 611.3<br>38 611.3                                                                           | 8 61<br>8 61<br>7 59                 | տատատ                                                                               | 37<br>37<br>37<br>37<br>37<br>37<br>37<br>59<br>50<br>73<br>50<br>73<br>50<br>73<br>50<br>73<br>50<br>73<br>50<br>73<br>50<br>73<br>50<br>73<br>74<br>75<br>75<br>75<br>75<br>75<br>75<br>75<br>75<br>75<br>75<br>75<br>75<br>75 |                                                                                         | 37<br>37<br>37<br>59<br>7<br>59<br>7<br>59<br>7                                                          |
| 11<br>11<br>11<br>11<br>11                                                                                 | 2 2 2 2 2<br>2 2 4 2                 | 00000                                                                               | 3 3 3 3 1 0<br>3 4 4 3 2 1 0                                                                                                                                                                                                     | 8 8 8 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                 | ተ ርዕ ርዕ ቀ ቁ ቁ<br>ተ ርዕ ርዕ ቀ ቁ ቁ                                                                           |

## ALIGNMENTS

| RESULT<br>Q813Q3 | LT 1<br>Q3                |                                                  |                           |          |                                                                                                                                    |
|------------------|---------------------------|--------------------------------------------------|---------------------------|----------|------------------------------------------------------------------------------------------------------------------------------------|
| A ID             | Q813Q3<br>Q813Q3;         | PRELIMINARY;                                     | PRT;                      | 2054 AA. | AA.                                                                                                                                |
| E E              | 01-MAR-2003               | (TrEMBLrel, 23,                                  | Creat                     | d)       | ed)                                                                                                                                |
| i L              | 01-MAR-2003               | (TrEMBLrel. 23,                                  | Last                      | nnotati  | sequence update)                                                                                                                   |
| E E              | Hypothetical<br>PFE1045C. | protein.                                         |                           |          |                                                                                                                                    |
| SO               | Plasmodium f              | Plasmodium falciparum (isolate 3D7)              | late 3D7                  |          |                                                                                                                                    |
| 8                | Eukaryota, A              | lveolata; Apic                                   | omplexa;                  | Haemos   | Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.                                                                       |
| N N              | NCB1_Tax1D=36329;<br>[11] | 6329;                                            |                           |          |                                                                                                                                    |
| RP.              | SEQUENCE FROM N.A.        | M N.A.                                           |                           |          |                                                                                                                                    |
| æ                | Devlin K., B              | aker S., Davie                                   | s P., Mun                 | ngal K.  | , Berriman M., Pain A.,                                                                                                            |
| R.               | Hall N., Bow              | man S., Church                                   | er C., O                  | lail M.  | Hall N., Bowman S., Churcher C., Quail M., Barrell B.;                                                                             |
| 12 2             | Submitted (S              | EP-2002) to th                                   | e EMBL/G                  | enBank/i | ODBJ databases.                                                                                                                    |
| Z I              | [7]                       |                                                  |                           |          |                                                                                                                                    |
| e<br>E           | SEQUENCE FROM N.A.        | M N.A.                                           |                           |          |                                                                                                                                    |
| ☆.               | MEDLINE=2225              | MEDLINE=22255708; PubMed=12368867;               | 2368867;                  |          |                                                                                                                                    |
| Æ                | Hall N., Pai              | n A., Berriman                                   | M., Chui                  | rcher C  | Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,                                                                  |
| æ                | Mungall K.,               | Bowman S., Atk                                   | in R., Ba                 | aker S., | , Barron A., Brooks K.,                                                                                                            |
| æ                | Buckee C.O.,              | Burrows C., C                                    | herevach                  | i., 유    | illingworth C.,                                                                                                                    |
| æ                | Chillingwort.             | h T., Christod                                   | onlou Z.,                 | . Clark  | Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,                                                                 |
| æ                | Cronin A., D              | avies R., Davi                                   | в Р., De                  | ar P., 1 | Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,                                                                   |
| Æ                | Feltwell T.,              | Goble A., Goo                                    | dhead I.,                 | . Gwill: | lam R., Hamlin N., Hance Z.,                                                                                                       |
| Ø.               | Harper D., H              | auser H., Horn                                   | sby T., I                 | tol royd | Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,                                                                         |
| <b>2</b> :       | Humphray S.,              | Jagels K., Ja                                    | mes K.D.,                 | Johnse   | Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,                                                                      |
| 4 4<br>2 0       | Ind A Mad                 | Kontortov B.,                                    | Kyes S.,                  | Larke 1  | Knights A., Komfortov B., Kyes S., Larke N., Lawson D., Lennard N.,<br>Line A. Maddison M. Molesn J. Money, D. Money, C. Money, J. |
| <b>2</b>         | Oliver K. O               | rmond D. Pric                                    |                           | M. M. A. | Oliver K. Ormond D. Price C. Ohail M.A. Rabbinowitsch F.                                                                           |
| . ₹              | Rajandream M              | .A., Rutter S.                                   | , Rutherf                 | ord K.   | 1., Sanders M., Simmonds M.,                                                                                                       |
| Z.               | Seeger K., S.             | harp S., Smith                                   | R., Sque                  | ares R., | quares S.,                                                                                                                         |
| \$:              | Taylor K., T              | Taylor K., Tivey A., Unwin L., Whitehead S.,     | L., Whit                  | ehead    | S., Woodward J.,                                                                                                                   |
| <b>5</b> 5       | Suiston J.E.              | Suiston J.E., Craig A., Newbold C., Barrell B.G; | wbold C.,                 | Barre    |                                                                                                                                    |
| 抗                | Nature 419:5              | 27-531 (2002).                                   | rarciparum curomosomes L, | STI OHIO | somes I, 3-y and 13.";                                                                                                             |
| ਲ.               | EMBL; AL9293              | EMBL; AL929353; CAD51573.1;                      |                           |          |                                                                                                                                    |
| <u>₹</u>         | Hypothetical protein.     | protein.                                         |                           |          |                                                                                                                                    |

Gaps

ô

```
STRAINSATCC 35092 / DSM 1617 / P2;
STRAINSATCC 35092 / DSM 1617 / P2;
STRAINSATCC 35092 / DSM 1617 / P2;
She Qi, Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jöng I., Jeffriss A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
                                                                                                       Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 16; Length 259; Pred. No. 22; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SMOG70; FING; 1.
Hypothetical protein; Protein; SEGURENCE 130 AA; 15106 MW; SBOB966B366BD159 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 1
Pred. No. 24;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8E3E1;
01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. EMBL, AE006804; AAK42162.1; - PIR, C90363; C90363; PIR. Interpro; IPR002716; PIN. Interpro; IPR006596; PINC. Pfam; PF01850; PIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein SSO1970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.vv,
                                                                                           Serotype M3;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 ITKYDYEFVY 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||
LTYYDASYAY 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2001 (
01-OCT-2001 (
01-JUN-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8E3E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q97WY9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
Q8E3E1
ID Q8E3E
AC Q8E3E
DT 01-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
Q97WY9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SON DREAD OF READ OF STREET OF STREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefes S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Rapur V., Daly J.A., Veasy L.G., Musser J.M.; Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks.";
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22133808; PubMed=12122206; Berotype M3; Beres S.B., Sylva G.L., Barblan K.D., Lei B., Hoff J.S., Barkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Cornievert P.M., Musser J.M.; Genome sequence of a serotype M3 strain of group A Streptococcus: emergence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.4%; Score 43; DB 16; Length 259; 70.0%; Pred. No. 22; ive 1; Mismatches 2; Indels
                                                                   Length 2054;
                                          Score 44; DB 5; Length 203-
Pred. No. 1.3e+02;
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes (serotype M18).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 24, Last annotation update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SpyM3_1272.
SpYM3_1272 OR SPS0590.
Streptococcus pyOgenes (serctype M3).
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
               2054 AA; 244096 MW; 522D7E233ACD1D1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
EMBL, AE010071; AAL9811.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 259 AA; 30329 NW; 40790BA21E3AC18B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein spyM18_1578.
                                                                                                                                                                                                                                                                                                                                                                                         259 AA.
                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
                                                                      71.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 70.0
Matches 7; Conservative
                                                                                                 Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                        |||||| : |
1046 LTYYDYNYDY 1055
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 ITKÝDÝEFVÝ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LTYYDYEFAY 11
                                                                                                                                                                                      2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=198466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=186103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus
               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        Q8P041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OBKENO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBK6N0
                                                                                                                                                                                                                                                                                                                                                                                         Q8P041
                                                                                                                                                                                                                                                                                                                            RESULT 2
0080041
0080041
0080041
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-00
01-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                         ò
```

ö

Gaps

.; 0

.; 0

Gaps

```
STACKLEN-CSTBL/64)

WEDLINE-22515520; PubMed=12628182;
WEDLINE-22515520; PubMed=12628182;
WEDLINE-22515520; PubMed=12628182;
WEDLINE-22515520; PubMed=12628182;
WEDLINE-22515520; PubMed=12628182;
WEDLINE-22515520; PubMed=12628182;
WEDLINE-CSTBL/64)

WE "Functional Expression of Murine V2R Pheromone Receptors Involves of Miccine Association with the M10 and M1 Families of MHC Class ID MOLECULES.";

WE Cell 112:607-618(2003)

WE MEDL, WY211079; AAO42745.1; -.

RE GO; GO:0016220; C:membrane; IEA.

GO; GO:0016220; C:membrane; IEA.

RE GO; GO:0016220; C:membrane; IEA.

RE GO; GO:0016220; C:membrane; IEA.

RICE-PRO; IPR003100; Ig-11ke.

RE INTER-PRO; IPR003100; Ig-11ke.

RE THER-PRO; IPR001039; MHC_I:

RE FAm; PP00047; IG: 1.

RE FAM; SM00407; IGC: 1.

RE ROSITE; PS00835; IG_LIKE; 1.

PROSITE; PS00835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Major histocompatibility complex class Ib M10.1 (Fragment).
                                     66.1%; Score 41; DB 16; Length 210; 60.0%; Pred. No. 39; 1; Indels ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER 1 -1
SEQUENCE 323 AA; 37016 MW; CDDB8C3C1D816828 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Histocompatibility 2, M region locus 10.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.5%; Score 40; DB 7; 87.5%; Pred. No. 89; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1] SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Vomeronasal organ;
MEDLINE=22507899; PubMed=12620187;
                                 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                |||::|:|
12 LTYFEYDFDY 21
                                                                                                                                                              2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 LTÝYGÝEF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LTYYDYEF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q85ZW9
Q85ZW9;
                                                                                                                                                                                                                                                                                                                                                                                                                       Q860W8;
                                                                                                                                                                                                                                                                                                                                                                                  Q860W8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                         RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                                                                                                                                                OS SZW9
OB PAC OS PAC O
                                                                                                                                                                 ò
                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=2603 V/R / Serctype V;
STRAIN=2603 V/R / Serctype V;
STRAIN=2603 V/R / Serctype V;
MEDLINE=22222988; PubMed=12206547;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Bennan M.J., Brinkac L.M., Daugherty S.C., DeBOY R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iscobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Fraser C.M., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                  STRAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
EMBL: ABD14272; AAN00638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 16; Length 210;
Pred. No. 39;
3; Mismatches 1; Indels
                                                                                                                            Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus agalactiae (serotype V).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sagalist, gbs1818; -.
InterPro; IPR007373; TPK_B1_binding.
InterPro; IPR007371; TPK_Catalytic.
Pfam; PF04265; TPK_B1_binding, 1.
Pfam; PF04263; TPK_Catalytic; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 210 AA; 23835 MW; 203E6B6FBBC81638 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007373; TPK B1 binding.
InterPro; IPR007371; TPK catalytic.
Pfam; PF04265; TPK B1 binding; 1.
Hypothetical protein; Complete protecome.
SEQUENCE 210 AA; 23890 MW; 7F9B91304B37B63E CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
GBS1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OBDXS1;
0-WRR-2003 (TrEMBLrel. 23, Created)
01-WRR-2003 (TrEMBLrel. 23, Last sequence update)
01-WRR-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invasive neonatal disease.",
Mol. Microbiol, 45:1499-1513(2002).
EMBL, AL766853; CAD47477.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conserved hypothetical protein. SAG1775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||::|:|
LTYFEYDFDY 21
                                                                                                                                                                                                                          NCBI_TaxID=216495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=216466;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                            Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunst F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8DXS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
QBDXS1
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDTDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDTDDTTDDTDDTTDDTDDTTDDDTTDDTDDTTDDTDDTTDDTDDTTDDTDDTTDDTDDTTDDTDDTTDDTDDTTDDTDDTTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDDTDDDTDDTDDTDDTDDTDDDTDDDTDDTDDDTDDDTDDDTDDDTDDDTDDDTDDDTDDDTDDDTDDDTDDDTDDDTDDDTDDDTDDDTDDDTDDD
```

ö

Gaps

```
Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 SVTYYQYEF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALTYYDYEF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q89YL8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
Q89YL8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
Ishii T., Hirota J., Mombaerts P., "Combinatorial Coexpression of Neural and Immune Multigene Families in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=2299266; PubMed=12705866;

Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,

Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pamunzio N.R.,

Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,

Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,

Hatfull G.F.,

"Origins of highly mosaic mycobacteriophage genomes.";

Call 113:171-182(2003).

EMBL, AX12932; AANON331.1; -.

SEQUENCE 77 AA, 8809 MW; B8D295DB02C82ED6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacteriophage Bxz2.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
VCBI_TaxID=205870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                     64.5%; Score 40; DB 7; Length 329; 87.5%; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 9; Length 77;
Pred. No. 30;
2; Mismatches 2; Indels
                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2310003L06Rik protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 495 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                  Mouse Voneronaeal Sensory Neurons.";
Curr. Biol. 13:394-400(2003).
EMBL, AFS59598, AAG5021.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016025; P:immune response; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003069; Ig-MHC.
InterPro; IPR003069; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALTYYDYBFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:| |:| |
48 AITDYNYELAY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 LTYYGYEF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LIYYDYEF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S:
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9CV82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q857E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9CV82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
09CV82
DD 09CV8
DT 01-JU
DT 01-JU
DE 23100
GN 23100
GN 23100
GN EMBE OC EMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
2085785
2085785
AC 0857
DD 01-0
DT 01
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
SEQUENCE FROM N.A.

STRANS-STEEL/60; TISSUE=TONGUE;

STRANS-STEEL/60; PubMed=11217651;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A. Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Asato T., Okazaki Y., Gojobori T., Bono H., Kaaukawa T., Saito R.,

A saito T., Matsuda H.A., Ashburner M., Beralov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomite M., Wagner L., Washio T.,

Schriml L.M., Staubli F., Suzuki R., Tomite M., Washio T.,

Blake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Pelcher C., Fulita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanoto N.,

Sasaki H., Toyo-oka K., Schoenbach C., Shibata Y., Storch K.-F.,

Rymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashiaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12663928;
Xu J. Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Bacteroidetes, Bacteroides (class), Bacteroidales, Bacteroidaceae, Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 62.9%; Score 39; DB 16; Length 580; Best Local Similarity 77.8%; Pred. No. 2.4e+02; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 11; Length 495;
Pred. No. 2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probom; PD004078; eIFS eIF28; 1.

Hypothetical protein; Complete proteome.
SEQUENCE 580 AA; 65978 MW; E6B0C88B3017922E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55471 MW; 1FE76D923CEDE9E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AKO09122, BABB6687.1, -.
MGD, MGI:1921498, 2310003L06Rik.
NON TER 495 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteroides thetaiotaomicron.
```

ഹ

```
SEQUENCE FROM N.A.

STRAIN=ATCC 33313 / NCPPB 528;

KN MEDLINE=21022145; PubMed=12024217;

Ad Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A da Silva A.C.R., Ferro J.A., Reinach F.C., Camargo L.B.A.,

Alwes L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Carrelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Carrelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Ratia J.B., Ferreira A.J.S., Ferreira R.C., Ferro M.T.T.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

A fordil B.C., Machado M.A., Madeira A.M.B.N., Martinez Rossi N.M.,

Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamiura R.E., Teixeira E.C., Tezza R.I.D.,

Trindade dos Santos M.A., Traid S.M., White F.F.,

Sctubal J.C., Kitajima J.P.;

Moreira L.M., White F.F., Takita M.A., Tamiura R.E., Moon D.H.,

Pereira J.G., Kitajima J.P.;

Moreira J.W., White F.F., Tesza R.I.D.,

Sctubal J.C., Kitajima J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Setubal J.C., Kitajima J.P.; "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUB=Pituitary,
Peinado J.R., Castano J.P., Sanchez-Hormigo A., Anouar Y., Tonon M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana ridibunda (Laughing frog) (Marsh frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
VCEL_TaxID=8406;
                                                                                                                                                                                                                           Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 16; Length 255;
Pred. No. 1.5e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 AA; 29205 MW; FD0C8C0570E8B71C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)
                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 AA
                                                                                                               255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE012359; AAM41756.1; -. GO; GO:0009405; P:pathogenesis; IEA. InterPro; IPR04357; IVSec_cagX. Pfam; FF03524; cagX; 1. Complete proteome. SEQUENCE 255 AA; 29205 MW; FD0C8C
                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.3%;
66.7%;
                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.,
                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 417:459-463 (2002)
                               55
2 LIYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYYDYDYA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LTYYDYEFA 10
                           LTLYDYELDY
                                                                                                                                                                                               VirB9 protein.
VIRB9 OR XCC2480.
                                                                                                                                                                                                                                                                               NCBI_TaxID=340;
                               46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162
                                                                                                               08P7X5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8JGW5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
Q8JGW5
                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                       Amsacta moorei entomopoxvirus (AmEPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=13 / Type A;
MEDLINE=21664373; PubMed=11792842;
Shimizu T., Ohtanni K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                             "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus: Analysis and Comparison with Other Poxviruses."; Virology 274:120-139(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,

MOYDER R.W.,

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF250284; AAG02808.1; -

SEQUENCE 148 AA; 18636 MW; DAA4C41A79AF04DZ CRC64;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=20396580; PubMed=10936094;
Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.3%; Score 38; DB 16; Length 154; 70.0%; Pred. No. 89; 2ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 12; Length 148;
Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL, AP003189; BAB8084.1.; -
Hypothetical protein; Complete protecme.
SEQUENCE 154 AA; 17870 MW; E8370264C4F9B7A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CPE1098.
                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                 148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                Created)
                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.3%;
50.0%;
                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50...
5; Conservative
                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : ||||:: |
137 MEYYDYKYIY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
                           162 TYYDYPRAY 170
3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LTYYDYEFAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               NCBI_TaxID=28321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             flesh-eater.";
                                                                                                                                                                                               AMV102.
                                                                                                             09 EMU7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8XLE4
                                                                                                                                                                                                               AMV102
                                                                          RESULT 12
Q9EMU7
                                                                                                                                ઠ
                             유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ે
```

ô

Gaps

. 0

```
RA Vaudry H., Gracia-Navarro F., Malagon M.M.;

E. Submitted (JAN-2002) to the EMEL/GenBank/DDBJ databases.

C. -- CATIVITY. D-GIVERALDEHYDB 3.PHOSPHATE + PHOSPHATE +

C. -- TATALYIC CATIVITY. B-GIVERALDEHYDB 3.PHOSPHATE + PHOSPHATE + NADH.

C. -- SUBCELLUAR SECOND PHASE OF GIVCOLYSIS, FIRST STEP.

C. -- SUBCILLUAR LOCATION: CYTOPLASHIY.

C. -- SUBCILLUAR LOCATION: CYTOPLASHIY.

C. -- SUBCILLUARS FAMILY.

DEHYDROGENSE FAMILY.

C. -- SIMILARITY: BELONGS TO THE GIVCERALDEHYDE 3-PHOSPHATE

DR GO, GO.0004365; F.Glyceraldehyde-3-phosphate dehydrogenase (p. . ; IEA.

DR GO, GO.0004365; F.Glyceraldehyde-3-phosphate dehydrogenase (p. . ; IEA.

DR GO, GO.0004365; F.Glyceraldehyde-3-phosphate dehydrogenase (p. . ; IEA.

DR THORPEO, PROMONA; GAPDH-I.

DR FAMI, PROMON4; GAPDH-I.

DR FAMI, PROMON4; GAPDH-I.

DR PRINTS; PROMON4; GAPDH-I.

DR PROSITE; PROMON13; GAPDH-I.

DR PROMON GAPTH GAPTH-I.

DR PROMON GAPTH
```

Search completed: October 6, 2004, 16:33:52 Job time : 41.8596 secs

2 LTYYDYEFAY 11 :|:|| || || 309 ITWYDNEFGY 318

g

à

OM protein

Run on:

```
Thu Oct 14 09:36:59 2004
```

```
US-VOY-VBK-BS-30

Sequence 30, Application US/09798689

PUblication No. US2033010397A1

GENERAL INFORMATION:

APPLICANT: Rockwell, Fatricia

APPLICANT: Rockwell, Fatricia

APPLICANT: Goldstein, Neil I.

TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE SEPRENCE: Sequence Listings 1-41 for 381-25 CIP

CURRENT APPLICATION NUMBER: US/09/798,689

CURRENT PILING DATE: 1097-10-10

PRIOR APPLICATION NUMBER: 08/967,113

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 08/706,804

PRIOR APPLICATION NUMBER: 08/706,804

PRIOR PLING DATE: 1996-09-03

PRIOR FILING DATE: 1996-00-07

PRIOR APPLICATION NUMBER: 08/706,804

PRIOR FILING DATE: 1994-10-20

PRIOR PRIOR APPLICATION NUMBER: 08/326,552

PRIOR APPLICATION NUMBER: 08/196,041

SOFTWARE: PATENTING DATE: 1994-10-20

PRIOR APPLICATION NUMBER: 08/326,552

PRIOR APPLICATION NUMBER: 08/326,552

PRIOR APPLICATION NUMBER: 08/326,552

PRIOR APPLICATION NUMBER: 08/196,041

SOFTWARE: PATENTING DATE: 1994-10-210

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PATENTING DATE: 1994-10-210
                                                                                                                                                                                                                          Sequence 26, Appl
Sequence 27, Appl
Sequence 29, Appl
Sequence 20, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 79, Appl
Sequence 41987, A
Sequence 41987, A
Sequence 2496, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 44, Seguence 2, A
                                                                                            Sequence
Sequence
Sequence
                                                                                                                                                                                  Sequence
                                                 Sequence
                                                                       Sequence
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 62; DB 10; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0015; Matches 11; Conservative 0; Mismatches 0; Indels
| US-10-374-531-118 |
| US-10-374-531-119 |
| US-10-374-531-119 |
| US-10-374-60-8 |
| US-10-374-600-13 |
| US-10-374-600-13 |
| US-10-374-600-13 |
| US-10-374-600-13 |
| US-10-374-600-24 |
| US-10-374-600-26 |
| US-10-374-600-27 |
| US-10-374-600-28 |
| US-10-374-600-29 |
| US-10-374-600-29 |
| US-10-374-600-29 |
| US-10-374-531-24 |
| US-10-374-531-27 |
| US-10-374-531-27 |
| US-10-374-531-30 |
| US-09-905-243-79 |
| US-09-905-244-79 |
| US-09-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALTYYDYEFAY 11
  ; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-198-689-30
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 111, App
Sequence 99, Appl
Sequence 99, Appl
Sequence 115, App
Sequence 117, App
Sequence 117, App
Sequence 117, App
Sequence 118, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 30, Appl
Sequence 6, Appli
                                                                                                                                                 ; Search time 68.5088 Seconds (without alignments) 51.669 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/ISO6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
                   15.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-798-689-30
US-09-96-954B-6
US-10-374-500-111
US-10-374-600-99
US-10-374-600-115
US-10-374-600-115
US-10-374-600-115
US-10-374-600-119
US-10-374-600-119
US-10-374-600-119
US-10-374-600-119
US-10-374-600-119
US-10-374-600-119
US-10-374-600-119
US-10-374-600-119
US-10-374-600-119
US-10-374-531-115
US-10-374-531-115
                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                   1351062 segs, 321799191 residues
                GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                      - protein search, using sw model
                                                                                                                                                   October 6, 2004, 16:34:15
                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                        US-09-635-974A-6
62
                                                                                                                                                                                                                                                                                   1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                Scoring table:
```

Minimum DB e Maximum DB e

Database

Searched:

Score

Result No.

111111 111111

ö

ö

.. 0

Gaps

..

임

```
Sequence 111, Application US/10374531
| Sequence 111, Application US/10374531
| Publication No. US20040006212A1
| GENERAL INFORMATION:
| APPLICANT: Imclone Systems Incorporated, et al.
| TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INTERFERENTS INTERFERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPTRY: US
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM compatible
COMPUTER: IBM compatible
COMPUTER: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 62; DB 12;
100.0%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REPERRNCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 425-7200
           REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 111: US-10-374-600-111
REGISTRATION NUMBER: 31,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-Feb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425-5288
                                                                                                                                         425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                      LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 425-52
INFORMATION FOR SEQ ID NO: 111:
                                                                                                                                            TELEFAX: (212) 425-52 INFORMATION FOR SEQ ID NO: 111: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALTYYDYBFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-374-531-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                            Sequence 6, Application US/09996954B
; Sequence 6, Application US/09996954B
; Publication No. US20030157104A1
; GENERAL INFORMATION:
    APPLICANT: Waksal, Haratment of Refractory Human Tumors
    TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
    TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
    TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
    TITLE OF INVENTION: WITH Epidermal Growth Factor Receptor Antagonists
    TITLE OF INVENTION: WITH Epidermal Growth Factor Receptor Antagonists
    CURRENT FILING DATE: 09/940,146
    PRIOR FILING DATE: 04-24-2001
    PRIOR FILING DATE: 08-13-1999
; PRIOR FILING DATE: 08-13-1999
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NOS: 12
; SEQ ID NOS: 12
; SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-10-374-600-111
; Sequence 111, Application US/10374600
; Publication No. US20030224001A1
; GENERAL INFORMATION:
; APPLICANT: Imclone Systems Incorporated, et al.
; APPLICANT: Imclone Systems Incorporated, et al.
; TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGWENTS FOR INPERTING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 62; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: 1BM compatible COMPUTER: Wordperfect NS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,600

FILING DATE: 25-Feb-2003

CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/08/973,065C FILING DATE: 19-MAY-1998 APPLICATION NUMBER: PCT/US96/09847 FILING DATE: 07-JUN-1996 APPLICATION NUMBER: US 08/482,982 FILING DATE: 07-JUN-1995 APPLICATION NUMBER: US 08/573,289 FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Deborah A. Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens-Rodent Chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALTYYDYEFAY 11
       ALTYYDYEFAY 11
                                                                                                                 RESULT 2
US-09-996-954B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-996-954B-6
```

g

```
Dilication No. COLONIA GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: IMClone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS
INTEL OF INVENTION: INFIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 31,995
TELECOMUNICATION NUMBER: 31,995
TELECOMUNICATION NUMBER: 11245/46003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; HYPOTHETICAL: NO FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 99: US-10-374-531-99
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                  ; Sequence 99, Application US/10374531
; Publication No. US20040006212A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
COUNTRY: US
               2 ALTYYDYEFAY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ALTYYDYEFAY 12
                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 99, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: LBM compatible COMPUTER: LBM compatible COMPUTER: LBM compatible COMPUTER: LBM compatible CURRENT APPLICATION NUMBER: US/10/374,600 FILING DATE: 25-Feb-2003 CLASSIFICATION NUMBER: US/10/374,600 FILING DATE: 25-Feb-2003 CLASSIFICATION NUMBER: US/08/973,065C FILING DATE: 19-Mar-1998 APPLICATION NUMBER: US 08/482,982 FILING DATE: 07-JUN-1996 APPLICATION NUMBER: US 08/482,982 FILING DATE: 07-JUN-1996 APPLICATION NUMBER: US 08/482,982 FILING DATE: 15-DEC-1995 APPLICATION NUMBER: US 08/573,289 FILING DATE: 15-DEC-1995 ATTORNEY/AGENT INFORMATION: NUMBER: US 08/573,289 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     Query Match
100.0%; Score 62; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 62; DB 12; Length 13; Best Local Similarity 100.0%; Pred. No. 0.0018; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INPORMATION:
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-10-374-531-111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid strangers: not relevant TOPOLOGY: not relevant MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 425-7200
TELEFAR: (212) 425-5288
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 13 amino acids
                                                                                                                                                                                                                                                            1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                        1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10004
                                                                                                                                                                                                                                                                                                                                                                                                          US-10-374-600-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-374-600-99
                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                        셤
```

```
.
0
                                                                                                                                                                                                                           RESULT 7
US-10-374-600-115
US-10-374-600-115
; Sequence 115, Application US/10374600
; Publication No. US20030224001A1
; GENERAL INFORMATION:
; APPLICANT: Inclone Systems Incorporated, et al.
; TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR
Query Match 100.0%; Score 62; DB 15; Length 13; Best Local Similarity 100.0%; Pred. No. 0.0018; Matches 11; Conservative 0; Mismatches 0; Indels
```

;

Indels

1 ALTYYDYEFAY 11

```
100.0%; Score 62; DB 12; Length 119; 100.0%; Pred. No. 0.016; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 117, Application US/10374600

Publication No. US20030224001A1

GENERAL INFORMATION:

APPLICANT: Inclone Systems Incorporated, et al.

ITLE OF INVENTION: INTIBODY AND ANTIBODY FRAGMENTS FOR INHIBOTING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
APPLICATION NUMBER: PCT/US96/09847
APPLICATION NUMBER: PCT/US96/09847
                                                                                PRIOR DATE: 25-Feb-2003

FILING DATE: 25-Feb-2003

CLASSIFICATION : CURROWN-
PRIOR APPLICATION NUMBER: US/08/973,065C

APPLICATION NUMBER: US/08/973,065C

FILING DATE: 19-Mar-1998

APPLICATION NUMBER: US/08/9847

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/482,982

FILING DATE: 07-JUN-1995

ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           TELEBRAK: (212) 425-7200
TELEBRAK: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETCAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 116:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESSS:
ADDRESSES: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS
                                          SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 425-52 INFORMATION FOR SEQ ID NO: 116: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-374-600-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-374-600-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-10-374-600-116
Sequence 116, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: ImClone Systems Incorporated, et al.
Intle OF INVENTION: ANTIBODY AND ANTIBODY FRAMENTS FOR INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 119;
                                                                                                                                                                                   COMPUTER READBLE FORM:

COMPUTER READBLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: 1BM compatible
COPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION PATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/06/073 0650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
           INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 425-7200
TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

STRANDEDDESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

HYPOTHETICAL: NO
FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 115:

US-10-374-600-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
SIREET: One Broadway
CITY: New York
                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                     STREET: One Broadway
                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 ALTYYDYEFAY 108
                                                                                                                     CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALTYYDYEFAY 11
                                                                                                                                                                  COUNTRY:
```

엄

ö

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 62; DB 12; Length 119; 100.0%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 119, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: 18 compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:

NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                    ; INVESTIGATION ACIDED TYPE: ALTON ACIDED ACIDED TYPE: ALTON ACIDED ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 119:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 425-720
TELEFAX: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not rele
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 118
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALTYYDYBFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-10-374-600-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 62; DB 12; Length 119; Best Local Similarity 100.0%; Pred. No. 0.016; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US.10-374-600-118
US.10-374-600-118
Sequence 118, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: ImClone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INTELLIBUTION:
INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOTTWARE: Wordperfect CURRIN APPLICATION DATA:

APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: AUNROWN:

RIOR APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 10-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 10-JUN-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 11-JUN-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 11-JUN-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAWM: Deborah A. Somerville
REGISTRATION NUMBER: 11,995
REFERENCE/DOCKET NUMBER: 11245/46003
FILING PROMOTICATION INFORMATION:
FILEDHONE: (212) 425-7200
TELEPHONE: (212) 425-7200
TELEPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 ALTYYDYEFAY 108
```

ð g

```
Gaps
                                      Sequence 115, Application US/10374531
Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
APPLICANT: Inclone Systems FRAGMENTS FOR TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 116, Application US/10374531
; Publication No. US20040006212A1
; Publication No. US20040006212A1
; GENERAL INFORMATION:
APPLICANT: INCLORE Systems Incorporated, et al.
TILLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INVENTION: INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible compEATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 62; DB 15; 100.0%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION: VURNOMAN-
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: CT/US96/09847
FILING DATE: 07-UW-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UW-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-374-531-115
                                                                                                                                                                           NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                     ZIP: 10004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212)
                                                                                                                                                                                                                                                                   CITY: New York
RESULT 13
US-10-374-531-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-374-531-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                        100.0%; Score 62; DB 12; Length 119; 100.0%; Pred. No. 0.016; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 62; DB 12; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: IMCIONE Systems Incorporated, et al. IITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/973,065C FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847 FILING DATE: 07-UW-1996
APPLICATION NUMBER: US 08/482,982 FILING DATE: 07-UW-1995
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 120: US-10-374-600-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                        Sequence 120, Application US/10374600 Publication No. US20030224001A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 120: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10004
COMPUTER READABLE FORM:
                                             Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                               98 ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALTYYDYEFAY 11
                                                                                                                                     1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                RESULT 12
US-10-374-600-120
  US-10-374-600-119
```

ö

CORRESPONDENCE ADDRESS: ADDRESSEE: Kenyon & Kenyon

NUMBER OF SEQUENCES:

98 ALTYYDYEFAY 108

```
98 ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: October Job time: 68.5088 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 62; DB 15; Length 119; 100.0%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 117, Application US/10374531
Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                            CITY: New York
STATE: New York
COUNTRY: US
ZIF: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPEATING SYSTEM: Ms.DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERTING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION NUMBER: US/08/973,065C
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INCHEMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSPORT TO CONTROL OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 116:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: One Broadway
CITY: New York
STATE: New York
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-374-531-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-10-374-531-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

CURRENT APPLICATION DATA

```
## APPLICATION NUMBER: US/10/374,531

FILING DATE: 25-Feb-2003

FILING DATE: 10-Feb-2003

FILING DATE: 10-Fac-1996

## APPLICATION NUMBER: US/08/973,065C

FILING DATE: 07-JUN-1996

## ATORICATION NUMBER: US 08/482,982

## ATORICATION NUMBER: US 08/482,982

## ATORICATION NUMBER: US 08/573,289

## ATORICATION NUMBER: 11,995

## ATORICATION NUMBER: 11,995

## REGISTRATION NUMBER: 11,995

## REGISTRATION NUMBER: 11,995

## ATORICATION  100 08; SCOTE 62; DB 15; Length 119;

## ATORICATION NUMBER: 11,995

## ATTORICATION NUMBE
```

This Page Blank (uspto)

```
6, 2004, 16:24:54; Search time 19.4912 Seconds (without alignments) 29.135 Million cell updates/sec
                                                                                                                                                                                                                                                                                                        389414
 5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                      389414 segs, 51625971 residues
GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum:Match 100%
Listing first 45 summaries
                                                            using sw model
                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                       US-09-635-974A-6
62
1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                            protein search,
                                                                                              October
                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                         Title:
Perfect score:
                                                              1
                                                              OM protein
                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                      Searched:
                                                                                            on:
                                                                                            Run (
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Issued Patents AA.\*

1. /ogTa\_6/ptodata/2/iaa/5A\_COMB.pep.\*
2. /ogTa\_6/ptodata/2/iaa/5B\_COMB.pep.\*
4. /ogTa\_6/ptodata/2/iaa/6A\_COMB.pep.\*
4. /ogTa\_6/ptodata/2/iaa/6B\_COMB.pep.\*
5. /ogTa\_6/ptodata/2/iaa/PCTUG\_COMB.pep.\*
6. /ogTa\_6/ptodata/2/iaa/PCTUG\_COMB.pep.\*

Database

Sequence 2, Appli Sequence 8, Appli Sequence 8, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 13, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 17, Appli Description US-08-800-198-2 US-09-296-595-2 US-09-296-595-8 US-08-369-822C-26 US-08-343-813-38 US-08-737-085A-2 US-09-839-666-2 US-09-839-666-1 US-09-838-1 US-09-838-1 US-09-838-1 US-09-838-1 US-09-838-1 US-09-838-1 US-09-838-1 US-09-838-1 US-09-846-258-1 US-08-737-085A-1 US-08-737-085A-1 US-08-737-085A-1 US-09-246-258-1 US-09-246-258-1 Query Match Length Score Result No. 

| Appl<br>Appl<br>Appl<br>Appl<br>Appl<br>Appl<br>Appl<br>Appl                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 0                         |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|
| 41.00.41.00.00.00.00.00.00.00.00.00.00.00.00.00                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Gaps                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Ga                        |
| Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Seq |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | .,                        |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                           |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 119<br>18                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ୍ଷ<br>ମ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | G)                        |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | RECEPTOR ANTIBODIE TE 1400 Version #1.30 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Length<br>; Inde          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | A THAT I                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | , Ľ                       |
| 114<br>114<br>117<br>118<br>119<br>119<br>119<br>119<br>119                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | EPTOR ANT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 7                         |
| S. 09-532-106-17<br>S. 09-532-106-17<br>S. 09-532-106-18<br>S. 09-532-106-18<br>S. 09-839-66-114<br>S. 09-839-66-114<br>S. 09-839-66-114<br>S. 09-839-66-114<br>S. 09-532-106-19<br>S. 09-532-106-18<br>S. 09-532-106-18<br>S. 09-246-258-18<br>S. 09-246-258-18<br>S. 09-246-258-18<br>S. 09-246-258-18<br>S. 09-246-258-18<br>S. 09-246-258-18<br>S. 09-246-258-18<br>S. 09-246-258-18<br>S. 09-246-258-18<br>S. 09-246-258-18                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | MENTS ECEPTOR E BRANICE 1400                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | DB<br>2;                  |
| 111000010000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ALIGNMENT ELIA TOR RECEP TOR RECEP SUITE 14 SUITE 14 0,198 1.576                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ; Di                      |
| 0.000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | I.I.GUM. S. O. V. UITE 198 5776                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | No.                       |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Score<br>Pred.            |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ALIGAS  800198 S. AS EVANGELIA GLAS H FACTOR E, ZELANO BLVD. SUI (k)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sc<br>Pr<br>1,            |
| <b>まままみははなるままなるままま</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | SULT 1  -08-800-198-2  Sequence 2, Application US/08800196  BREAT NO. 594260.  APPLICANT: WELS, WINFRIED S.  APPLICANT: SCHMIDT, MATHIAS  APPLICANT: ALINGTON WITE, ZEI  STREET: Z200 CLARENDON BLUD.  STRATE: VA  CONMUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: PATENTIN PC-DOS/MS-I  SOFTWARE: PATENTIN PC-DOS/MS-I  COMPUTER: PATENTIN PC-DOS/MS-I  SOFTWARE: PATENTIN PC-DOS/MS-I  SOFTWARE: PATENTIN PC-DOS/MS-I  SOFTWARE: AMLET-KING, DIANA  REGISTRATION NUMBER: 33,302  REFERENCE/DOCKET NUMBER: SCH  TELEFONE: 703-243-6410  INFORMATION FOR SEQ ID NO: 2:  SEQUENCE CHARACTERISTICS:  LEBNOTH: 119 amino acide  STRANDENNES: SINGL  TYPE: amino acid  STRANDENNES: NO  ANTI-SENSE: NO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 40 A0                     |
| 77777777777777777777777777777777777777                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | S C C C C C C C C C C C C C C C C C C C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 45.0<br>40.0              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ion US/  WINERI WINERI WINERI LODOT, MAT LOD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 6<br>7<br>vati            |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Cation:  10.  10.  10.  10.  10.  10.  10.  10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 8 Z                       |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | TILICAT<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATION<br>MATIO                                                                                                          | .larity<br>Conserv        |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | -2<br>APP1i<br>SCRMATO<br>T SCRMATO<br>T SCRMATO | II S                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Hence 2, Applent No. 5942  Hence 2, Applent No. 5942  Hence 2, Applent No. 5942  APPLICANT: WAPPLICANT: WAPPLICANT: SAPPLICANT: SAPPLICANT: SAPPLICANT: SAPPLICANT: SAPPLICANT: SAPPLICANT: SAPPLICANT: SAPPLICANT: WAPPLICANT: WAPPLICANTER: COMPUTER: COMPUTER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | . S. F.                   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | LEGRAL OF LEGRAL OF LEGRAL NO LOGARD OF LOGARD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | tch<br>3al                |
| ,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TIT 1<br>NUMBER 1<br>STITE STITE S                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | y Matci<br>Local<br>hes   |
| 220mmmmmmmm44444<br>86012m45970012m45                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | NULT APPROVED THE NUMBER OF TH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Query<br>Best I<br>Matche |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | RESULT 1  US-08-800-198-2  Sequence 2, Application US/08800199  Sequence 2, Application US/08800199  BAPLICANT: WELS, WINFRIED S.  APPLICANT: SCHMIDT, MATHIAS  APPLICANT: SCHMIDSES: 17  CORRESPONBENCES: 17  CORRESPONBENCES: 17  CITY: ARLINGTON  STATE: VA  COUNTRY: US  ZIP: 22201  STATE: VA  COMPUTER: EMP PC compatible  OMPUTER: EMP PC compatible  OMPUTER: PATHINGTON  MEDIUM TYPE: Floppy disk  COMPUTER: BER PC compatible  OMPUTER: PATHINGTON  SOFTWARE: PATHIN PATH  APPLICATION DATA:  APPLICATION NUMBER: SCH PATHING DIANA  REGISTRATION SYSTEM: 33,302  REFERENCE/DOCKET NUMBER: SCH  TELEFAX: 703-243-643  STRANTION FOR SEQ ID NO: 2:  SEQUENCE CHARACTERISTICS:  LENGTH: 119 amino acide  TOPOLOGY: linear  MOLECULE TYPE: NO  ANTI-SENSE: NO  SRAGNENT TYPE: Internal  US-08-800-198-2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Aae                       |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Ди и и и и и и и и и и и и и и и и и и                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                           |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                           |

---

g

```
Sequence 26, Application US/08369822C
Sequence 26, Application US/08369822C
Sequence 26, Application US/08369822C
GENERAL INFORMATION:
JAPLICANT: Libkin, W. I.
APPLICANT: Libkin, W. I.
APPLICANT: Strick A.
APPLICANT: Schneemann, Anette
TITLE OF INVENTION: Borne Disease Viral Sequences,
TITLE OF INVENTION: Diseases
TITLE OF INVENTION: System Diseases
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS: 46
CORRESPONDENCE ADDRESS: 46
CORRESPONDENCE ADDRESS: AMOUNT OF THE COMMENT OF THE COM
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                      Score 39; DB 2; Length 240;
Pred. No. 25;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WELS, WINFRIED S.
APPLICANT: WELS, WINFRIED S.
APPLICANT: WARALOPOULOU, EVANGELIA.
APPLICANT: SCHNIDT, MATHIAS
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
FILE REFERENCE: SCH-1576 D1
CURRENT FAPLICATION NUMBER: US/09/296,595A
CURRENT FILING DATE: 1999-04-23
FEALIER APPLICATION NUMBER: 08/800,198
BARLIER APPLICATION NUMBER: 08/800,198
BARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VOT: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Fulbright & Jaworski, L.L.P.
865 South Figueroa Street, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 3;
Pred. No. 25;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09296595A Patent No. 6129915 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.9%;
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
LENGTH: 240 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                    MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-800-198-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 90017-2571
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 YYGYDFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 YYGYDFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                       4 YYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 YYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Los Angeles
California
                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PKT
ORGANISM: Murine sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-369-822C-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
ZIP: 9003
                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-296-595-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-296-595-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 3; Length 119;
Pred. No. 12;
1; Mismatches 1; Indels
                                                                                                                                                                                                                Sequence 2, Application US/0929555A

patent No. 612915

GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: WINTERD S.

APPLICANT: SCHMIDT, MATHIAS

TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES

TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES

CURRENT APPLICANTON NUMBER: US/09/296,595A

CURRENT FILING DATE: 1999-04-23

CURRENT FILING DATE: 1999-04-23

MUMBER OF SEQ ID NOS: 18

SEQ ID NO 2

LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08800198
PETENT NO: 5942602
GENERAL INFORMATION:
APPLICANT: WELS, WINFRIED S.
APPLICANT: SCHMIDT, MATHIAS
APPLICANT: SCHMIDT, MATHIAS
APPLICANT: SCHNIDER, DOUGLAS
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,198
FILING DATE: 13-PEB-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPERENCE/DOCKET NUMBER: 33,302
REPERENCE/DOCKET NUMBER: SCH
TELEDOWNUNICATION INFORMATION:
TELEPHONE: 703.243-6333
TELEPAX: 703.243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || |:|||
101 YYGYDFAY 108
                                                                            101 YYGYDFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 YYDYEFAY 11
                       YYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Murine sp. US-09-296-595-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
```

a

.. 0

```
RESULT 7
US-08-44-831B-38
US-08-44-831B-38
Sequence 38, Application US/08434831B
Patent No. 6113905
GENERAL INFORMATION:
APPLICANT: Libkin, W. I.
APPLICANT: Schneider, Patrick A.
APPLICANT: Schneemann, Anette
APPLICANT: Schneemann, Anette
TITLE OF INVENTION: Borna bisease viral Sequences,
TITLE OF INVENTION: System Diseases
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rulbright & Jaworski, L.L.P.
STREET: 865 SOUTH Figueroa Street, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 3; Length 509;
Pred. No. 81;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: FULDINGING & CANOISAL, L.L.F.
STREET & SOLUTION & CANOISAL, L.L.F.
CITY: Los Angeles
STATE: Galifornia
COUNTRY: USA
ZIP: 90017-2571
COMPUTER READABLE FORM:
MEDIUAT TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYTEM: MINDOWS NT-WORDPERFECT 8.0
SOFTWARE: ASCII (DOS) TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/434,831B
FILING DATE: 04-MAY-1995
CLASSIFICATION NUMBER: US 08/369,822
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CHUCCHIII, MATGATE A. (Ph.D.)
REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 39,944
                                          1279-194C2
   REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 1279
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213/892-920
TELEPHONE: 213/892-920
TELEPHONE: 213/892-920
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: 213/692-9200
INFORMATION FOR SEQ 10 NO: 36
SEQUENCE CHARACTERISTICS:
LENGTH: 509 anino acids
TYPE: anino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAY: NO
ANTI-SENSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.3
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446 TYFDSEFSY 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                  , ANTI-SENSE: NO
US-08-582-776C-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lipkin, W. I.
APPLICANT: Briese, Thomas
APPLICANT: Briese, Thomas
APPLICANT: Striche, Stefanie
APPLICANT: Schneider, Patrick A.
APPLICANT: Stitz, Lothar
APPLICANT: Schneemann, Anette
APPLICANTION: System Disease Viral Sequences,
TITLE OF INVENTION: System Disease
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 865 South Figueroa Street, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.3%; Score 38; DB 3; Length 509; 66.7%; Pred. No. 81; tive 2; Mismatches 1; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS NT-WORDPERFECT 8.0
SOFTWARE: ASCII (DOS) TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,822C
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CHURChill, Margaret A. (Ph.D.)
REGISTRATION NUMBER: 39,944
REFERENCY/DOCKET NUMBER: 1279-194XX
TELECOMMUNICATION INFORMATION:
TELEFAX: 213/892-9200
TELEFAX: 1000
TELEFAX: 1000
TELEFAX: 1000
TOPOLOGY: 10000
TYPE: maino acid
TOPOLOGY: 100000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 865 South Figueroa Street, 29 CITY: Los Angeles STATE: California COUNTRY: USA LOS Angeles STATE: CONFUTRY: USA LOS Angeles CONFUTRY: USA CONFUTRY: USA COMPUTER READABLE FORM: WINDOWN TYPE: Ploppy disk COMPUTER: USP FOR COMPATIBLE OF STATEM: WINDOWN NT SOFTWARE: ASCII DOS TEXT CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/582,776C FILING DATE: 04-JAN-1996 CLASSIFFCATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/369,822 FILING DATE: 06-JAN-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/434,831 FILING DATE: 04-WAY-1995 ATTORNEY/AGBNT INFORMATION: NAME: Churchill, Margaret A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-06-582-776C-41
; Sequence 41, Application US/08582776C
; Patent No. 6077510
; Patent No. 6077510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       446 TYFDSEFSY 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-369-822C-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
APPLICATION NUMBER: US/08/737,085A
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/737,085
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION:
TELEPHONE: 212-537-7659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 Third Avenue
CITY: New York
STATE: New York
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 70.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: peptide US-09-246-258-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LIYYDYEEDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                        CITY: Ne
STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                  Score 38; DB 3; Length 509;
Pred. No. 81;
                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08737085A

Fatent No. 586932

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSE:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09246258
; Patent No. 6040137
; GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: EXCHANGER
; TITLE OF INVENTION: EXCHANGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB Pred. No. 2.4; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3846/0C569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846,
TELECOMMUNICATION:
TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.7%;
70.0%;
                                             Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 236687
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 27-DEC-1
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS LENGTH: 13 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                             446 TYFDSEFSY 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIYYDYEEDY 12
                                                                                                                                                           3 TYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
US-08-434-831B-38
                                                                                                                                                                                                                                                                                          RESULT 8
US-08-737-085A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-737-085A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-09-246-258-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 3; Length 13;
Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10

10.09-532-106-2

1 Sequence 2, Application US/09532106

1 Patent No. 6245895

1 GENERAL INFORMATION:

APPLICANT: SALIBERG, MATTI

TITLE OF INVENTION: EXCHANGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTANE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/532,106
FILING DATE: 21-Amar-2000
PRIOR APPLICATION DATA:
ZIP: 10022
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5EQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/246,258
FILING DATE:
CLASSIFICATION:
```

```
Gaps
                                                         .
0
                  DB 4; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                             Sequence 1, Application US/08737085A
Patent No. 5869232
GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
TITLE OF INVENTION: EXCHANGER
NUMBER OF SEQUENCES: 23
CORRESPONDEC ADDRESS: ADDRESSES: DARBY PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09246258
Patent No. 6040137
GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
TITLE OF INVENTION: EXCHANGER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,085A
FILING DATE: 27-DEC-1996
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTOM DATE:
                Score 37; DB 4
Pred. No. 2.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 2
Pred. No. 2.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
Query Match
Best Local Similarity 70.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                          2 LTYYDYEFAY 11
                                                                                                                                  LIYYDYEEDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New Yor!
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                             ò
                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                 Query Match 59.7%; Score 37; DB 3; Length 13; Best Local Similarity 70.0%; Pred. No. 2.4; Matches 7; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRING APPLICATION DATA:
APPLICATION NUMBER: US/09/839,666
FILING DATE: 19-Apr-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09839666
Patent No. 6469143
GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: EXCHANGER
                          NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
TELEX: 23667
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUICATION INFORMATION:
TELEPHONE: 212-527-7659
TELEPHONE: 212-753-6237
                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-532-106-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION WHOBER: 08/737,085
FILING DATE: «UNKnown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
STRANDEDNESS: single
POPLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-839-666-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: DARBY & DARBY
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                        LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LIYYDYEEDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-09-839-666-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

·;

ø

us-09-635-974a-6.rai

```
Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.7%; Score 37; DB 4; Length 14; 70.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09839666
Patent No. 6469143
GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: EXCHANGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                59.7%; Score 37; DB 3; 70.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/839,666
FILING DATE: 19-Apr-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/737,085
FILING DATE: «Unknown»
ATTORNEY/AGENT INPORMATION:
NAME: Green, Reza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUTCATION INFORMATION:
TELEPHONE: 212-277-7659
TELEPRAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                         0, Mismatches
                                                                                                                                                           TYPE: anino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-532-106-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

NOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-839-666-1
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         & DARBY PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                              2 LTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LIYYDYEEDY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09532106
Patent No. 6245895
GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: EXCHANGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/532,106
FILING DATE: 21-Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/246,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/737,085A FILING DATE: 27-DEC-1996 ATTORNEY/AGENT INFORMATION: NAME: Green, Reza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/737,085
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECHONE: 212-527-7659
TELEPHONE: 212-527-7659
TELEPHONE: 212-537
TELEPHONE: 21687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.7%;
                      New York
New York
                                                                                                                                            1: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                              COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-09-246-258-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LIYYDYEEDY 12
      DARBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10022
                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
```

QD

0;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps Qy 2 LTYVDYEFAY 11

Db 3 LIYYDYEEDY 12

Search completed: October 6, 2004, 16:36:32
Job time: 20.4912 secs

This Page Blank (Usolo)

7

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

October 6, 2004, 16:20:48; Search time 55.5789 Seconds (without alignments) 55.921 Million cell updates/sec Run on:

US-09-635-974A-6 62 1 ALTYYDYEFAY 11 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\* 1: qeneseqp1980s:\* geneseqp1980s;\* geneseqp1990s;\* Database :

geneseqp2003as:\* geneseqp2003bs:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2004s: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description           | Aay59313 Heavy cha | 54 Anti-I | 984      |          | 950 Heavy |       | 951 | Aaw08954 Heavy cha | 7 Heavy  |          | 2 Heavy  |          | 'n       | Aaw05140 scFv2 (225 | თ        | _        | Abg10386 Novel hum | Abp28261 Streptoco |          | Ċ        | 5682 Huma | 1705     | Aab19745 Erythropo |          | Aab19747 Erythropo |
|-----------------------|--------------------|-----------|----------|----------|-----------|-------|-----|--------------------|----------|----------|----------|----------|----------|---------------------|----------|----------|--------------------|--------------------|----------|----------|-----------|----------|--------------------|----------|--------------------|
| ΩI                    | AAY59313           | AAB37954  | AAU77786 | AAW08953 | AAW08950  | Oυ.   | 95  | AAW08954           | AAW08947 | AAW08944 | AAW08942 | AAW05133 | AAW05135 | AAW05140            | AAW05139 | AAW05141 | ABG10386           | ABP28261           | AAB19756 | AAY56681 | AAY56682  | AAY56705 | AAB19745           | AAB19748 | AAB19747           |
| Length DB             | 11 3               | -         |          | თ        | 6         | 19    | 19  | 19                 | 38       | 38       | 138 2    | 40       | 651 2    | 92                  |          | 1020 2   |                    | _                  | _        | œ        | 19        | 20       |                    | 'n       | D.                 |
| %<br>Query<br>Match 1 | 100.0              | 0         | 100.0    | 0        | ö         | 100.0 | 0   | 100.0              | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    |                     | 100.0    | 100.0    | 67.7               | Ġ                  | 64.5     | 4.       | 4.        | 4.       |                    | 4.       | 4.                 |
| Score                 | 62                 | 62        | 62       | 62       | 62        | 62    | 62  | 62                 | 62       | 62       | 62       | 62       | 62       | 62                  | 62       | 62       | 42                 | 41                 | 40       | 40       | 40        | 40       | 40                 | 40       | 40                 |
| Result<br>No.         | 1                  | 7         | m        | 4        | w         | φ     | 7   | ω                  | o,       | 10       | 11       | 12       | 13       | 14                  | 15       |          | 17                 |                    |          |          |           |          | 23                 |          |                    |

| Aaw71240 Heavy cha | Aaw71243 scFv comp | Aar13721 Control É | Abm74082 DNA clone | Abm73723 DNA clone | Abp75850 Human sec | Adb64342 Human pro | Aar84527 CDRH3 of | Aar84526 CDRH3 of | Aaw38244 CDR3-H3 s | Aar84538 Anti-HIV- | Aar84539 Anti-HIV- | Aar84543 Anti-HIV- | Aar84548 Anti-HIV- | Aar84542 Anti-HIV- | Aar84544 2[Anti-HI | Aar84540 Anti-HIV- | Aar84541 Anti-HIV- |            | Aar48619 Sequence |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|-------------------|
| 2 AAW71240         | 2 AAW71243         | 2 AAR13721         | 7 ABM74082         | 7 ABM73723         | 6 ABP75850         | 7 ADB64342         | 2 AAR84527        | 2 AAR84526        | 2 AAW38244         | 2 AAR84538         | 2 AAR84539         | 2 AAR84543         | 2 AAR84548         | 2 AAR84542         | 2 AAR84544         | 2 AAR84540         | 2 AAR84541         | 4 ABG03953 | 2 AAR48619        |
| 119                | 240                | 120                | 322                | 471                | 561                | 815                | 13                | 14                | 14                 |                    |                    |                    | 24                 | 24                 |                    |                    | 56                 | 115        | 120               |
| 62.9               | 62.9               | 62.1               | 61.3               | 61.3               | 61.3               | 61.3               | 59.7              | 59.7              | 59.7               |                    | 59.7               | 59.7               | 59.7               | 59.7               | 59.7               | 59.7               | 59.7               | 59.7       | 59.7              |
| 8                  | <b>м</b>           | 38.5               | 38                 | 38                 | 38                 | 38                 | 37                | 37                | 37                 | 37                 | 37                 | 37                 | 37                 | 37                 | 37                 | 37                 | 37                 | 37         | 37                |
| 56                 | 27                 | 28                 | 29                 | 30                 | 31                 | 32                 | 33                | 34                | 35                 | 36                 | 37                 | 38                 | 33                 | 40                 | 41                 | 42                 | 43                 | 44         | 45                |

## ALIGNMENTS

Heavy chain hypervariable region, CDR3. AAY59313 standard; peptide; 11 AA 07-MAR-2000 (first entry) AAY59313; AAY59313 

Hypervariable region, complementarity determining region, CDR, tumour, single chain antibody, growth inhibitor, human, tumourigenesis, therapy, protein receptor tyrosine kinase, heavy chain.

WO9960023-A1. Mus sp.

99WO-US010741. 14-MAY-1999; 25-NOV-1999.

98US-00079612. 98US-0085613P. 98US-00206138. 15-MAY-1998; 15-MAY-1998; 07-DEC-1998;

Robert F, Buchsbaum DJ; (IMCL-) IMCLONE SYSTEMS INC. (UABR-) UAB RES FOUND. Waksal HW, Saleh MN,

WPI; 2000-062440/05. N-PSDB; AAZ48627.

Treatment of human tumors, using a combination of radiation and a non-radiolabeled protein receptor tyrosine kinase inhibitor.

Disclosure, Page 15; 31pp; English.

This sequence is the hypervariable region CDR3 (complementarity determining region 3) of the heavy chain of a single chain antibody derived from the murine antibody 225. The invention relates to a method for inhibiting the growth of tumours in human patients by treating with an effective amount of a combination of radiation and a non-radiolabelled protein receptor tyrosine kinase (PRTK) inhibitor, the overexpression of which can lead to tumourigenesis. The method can be used in the treatment of tumours of e.g. breast, lung, colon, kidney, bladder, head and neck, ovary, prostate or brain. The administration of a suitable antibody to

¥.

1 ALTYYDYEFAY 11

(first entry)

SXS

ò g

```
Mouse heavy chain hypervariable region (CDR3) of 225 antibody
                                                              AAU77786 standard; peptide; 11
                                                                                                       05-JUN-2002
                                                                                   AAU77786;
                                                                          셤
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a method for inhibiting the growth of refractory tumours that are stimulated by a ligand of epidermal growth factor receptor (BGFR) in human patients. The method involves treating the patient with a combination of BGFR/human EGF-1 (HER1) antagonist, optionally with a chemotherapeutic agent or radiation. The antagonist can BGFR/HRR1 attagonist is useful for inhibiting the growth of refractory tumours such as tumours of breast, heart, lung, small intestine, colon, spine, bone marrow, blood, thymus, uterus, testicles, cervix and liver, preferably squamous cell carcinomas. The present sequence represents the heavy chain variable region complementarity determining region 3 amino acid sequence of the chimeric anti-EGFR monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epidermal growth factor receptor/human epidermal growth factor receptor-1 antagonist for inhibiting the growth of refractory tumors.
                                                                                                                                                                                                                                                  Refractory tumour growth inhibition; epidermal growth factor receptor; EGFR antagonist; cancer; squamous cell carcinoma; anti-EGFR antibody; complementarity determining region; CDR.
                                                                Gaps
                                                                                                                                                                                                                              Anti-EGFR monoclonal antibody H chain V region CDR3 peptide sequence.
                                                                ..
the patient makes the tumour more susceptible to radiotherapy
                                          Length 11;
                                                              0; Indels
                                          100.0%; Score 62; DB 3; I
100.0%; Pred. No. 0.00041;
                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 13; 31pp; English
                                                                                                                                                               AAB37954 standard; protein; 11 AA.
                                                                ..
                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000; 2000WO-US011756.
                                                                                                                                                                                                                                                                                                                                                                                              99US-00374028,
                                                                                                                                                                                                                                                                                                                                                                                     99US-00312284
                                                                                                                                                                                                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                          12-MAR-2001 (first entry)
                                                     Local Similarity 100.
                                                                                     1 ALTYYDYEFAY 11
                                                                                                  WPI; 2001-016160/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC83237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                    WO200069459-A1.
                       Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                         23-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Waksal HW;
                                                                                                                                                                                     AAB37954;
                                            Query Match
                                                                                                                                                                                                                                                                                                Mus sp
                                                                Matches
                                                                                                                                                    RESULT 2
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel method for treating a mammal with hyperproliferative disease stimulated by a ligand of a member of the epidermal growth factor (EGP) family of receptors. The method involves administering an antibody or a defective receptor that is an antagonist of a member of the EGF receptor family, or a combination of the rantagonist and photocherapy, chemotherapeutic agent or radiation therapy. The attibody used in the method of the invention acts as an epidermal growth factor receptor (EGFR) antagonist by inhibiting EGFR /HERI phosphorylation. The method of the invention is useful for treating a mammal with hyperproliferative disease such as psoriasis, actinic keratoses, seborrheic keratoses, warts, keloid scars and eczema simulated by a ligand of a member of the EGF family of receptor. This sequence represents the mutine anti-EGF 255 antibody heavy chain (VH) hypervariable region (CDR3) used as an inhibitor of EGFR in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating a mammal with hyperproliferative disease especially psoriasis, stimulated by ligand of member of epidermal growth factor family of receptors, by administering antagonist of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Mouse; heavy chain; antibody; hyperproliferative disease; epidermal growth factor; EGF; psoriasis; actinic keratosis; seborrheic keratosis; warts; keloid scars; eczema; 255 antibody; hypervariable region; CDR3; EGFR inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th 100.0%; Score 62; DB 5; Length 11; Similarity 100.0%; Pred. No. 0.00041; 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW08953 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 12; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2000; 2000US-00635974.
                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001; 2001WO-US041647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMCL-) IMCLONE SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Η
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          디
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALTYYDYEFAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALTYYDYEFAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-257423/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABK11442.
                                                                                                                                                                                                                                                           WO200211677-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                          14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reufel T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
AAW08953
ID AAW0
XX
```

ö

Gaps

. .

Query Match
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 11; Conservative 0; Mismatches 0; Indels

1 ALTYYDYEFAY 11

Heavy chain; reshaped; monoclonal; antibody; 225RA; human; epidermal growth factor; BGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region, CDR.

36. .49 /label= framework\_2 50. .65 /label= CDR\_2 66. .97 /label= framework\_3

109. .119 \_\_\_/label= framework\_4

WO9640210-A1.

/label= CDR\_3

.108

1. .30 /label= framework\_1 31. .35 /label= CDR\_1 Location/Qualifiers

ното варіеля

Key Region Region Region Region Region Region Region

Heavy chain variable region of 225RA antibody.

(first entry)

18-SEP-1997

AAW08950;

```
Heavy chain; reshaped; monoclonal; antibody; 225RD; human; pepidermal growth factor; BGR; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostatic; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAb) H255, 225HB. The MAb is specific for the human motoclonal antibody (MAb) H255, 255HB. The MAb, so a fragment, can be used to inhibit the growth of tumour calls, especially late stage special to tumour calls in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saldanha JW;
                                                Heavy chain variable region of 225RD antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Giorgio NA, Jones ST,
                                                                                                                                                                                               31. .35

/label= CDR_1

/label= framework_2

50. .65

/label= CDR_2

6.97

/label= framework_3

98. .108
                                                                                                                                                                                                                                                                                                           /label= CDR_3
109. .119
/label= framework_4
                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                          l. .30
/label= framework_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 30; Fig 22; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-00482982.
95US-00573289.
                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US009847
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldstein NI,
                                                                                                                                                                                                                                                                                                                                                             WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1996;
                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
15-DEC-1995;
                        18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-1996
                                                                                                                                                             Key
Region
                                                                                                                                                                                                  Region
                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                           Region
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAb) H255, 225RA. The MAb is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage agent tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 62; DB 2; Length 119; 100.0%; Pred. No. 0.0056; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW08952 standard; protein; 119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 30; Fig 22; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
AAW08952
ID AAW0
XX
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

ô

Gaps

;

Indels

100.0%; Score 62; DB 2; Length 119; llarity 100.0%; Pred. No. 0.0056; Conservative 0; Mismatches 0; Indels

RESULT 5 AAW08950 1D AAW08950 standard; protein; 119 AA. XX

98

d 8

11

1 ALTYYDYEFAY

Saldanha JW;

Giorgio NA, Jones ST,

WPI; 1997-051897/05.

Goldstein NI,

(IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.

07-JUN-1995; 15-DEC-1995; 07-JUN-1996; 19-DEC-1996.

96WO-US009847 95US-00482982. tumour; cell;

AAW08952

Key Region Region Region Region Region Region Region

```
The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RHB. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                 Heavy chain; reshaped; monoclonal; antibody; 225RB; human; epidermal growth factor; EGF; receptor; inhibition; growth; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 62; DB 2; Length 119; 100.0%; Pred. No. 0.0056; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saldanha JW;
                                                        Heavy chain variable region of 225RB antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Giorgio NA, Jones ST,
                                                                                                                                                                                                                   1. .30
/label= framework_1
31. .35
/label= CDR_1
                                                                                                                                                                                                                                                                                6. .49
|label= framework_2
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           framework_3
                                                                                                                                                                                                                                                                                                                                                                                                           109. .119
/label= framework_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 30; Fig 22; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.001
100.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                         CDR_3
                                                                                                                                                                                                                                                                                                             50. .65
/label= CDR_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US009847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00482982.
                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                          98. .108
/label= C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108
                                                                                                                                                                                                                                                                                                                                           66. .97
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 ALTYYDYEFAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goldstein NI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1996;
                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9640210-A1
                             18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-1996
AAW08951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                     Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
\delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAb) H255, 225HC. The MAb is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                        Heavy chain; reshaped; monoclonal; antibody; 225RC; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 62; DB 2; Length 119; 100.0%; Pred. No. 0.0056; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saldanha JW;
                                                               variable region of 225RC antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                56. 97 __/label= framework_3
                                                                                                                                                                                                                                                                                  16. .49
'label= framework_2
                                                                                                                                                                                                     iocation/Qualifiers
                                                                                                                                                                                                                         .. .30
'label= framework 1
                                                                                                                                                                                                                                                                                                                                                                                                               109. .119
/label= framework_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 30; Fig 22; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                            98. 108
/label= CDR_3
                                                                                                                                                                                                                                                    11. .35
/label= CDR_1
                                                                                                                                                                                                                                                                                                              50. .65
/label= CDR_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US009847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-00482982.
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goldstein NI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                  18-SEP-1997
                                                             Heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-1996.
```

; 0

Gaps

.. 0

AAW08954 standard; protein; 119 AA.

AAW08954 ID AAWC XX

AAW08951 standard; protein; 119 AA.

RESULT 7
AAW08951
ID AAW0
XX

Matches

- nsed

(first entry)

```
Heavy chain, reshaped, monoclonal, antibody, 225RA, human, epidermal growth factor, EGF, receptor, inhibition, growth, tumour, cell, late stage, prostatic, prostate, variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAb) H252, 228HA. The MAb is specific for the human monoclonal antibody (MAb) H252, 228HA. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                           Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                         Heavy chain variable region of 225RA antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 31; Fig 20; 112pp; English.
                                                                                                                                                                                                                                                                                 (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT49346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 138 AA;
                                                                                                                                                                                                                                                                                                                          Goldstein NI,
                                                                                                                                        Homo sapiens
                                                                                                                                                              WO9640210-A1
                                                                                                                                                                                                                   07-JUN-1996;
                                                                                                                                                                                                                                           07-JUN-1995;
15-DEC-1995;
                              18-SEP-1997
                                                                                                                                                                                         19-DEC-1996,
     AAW08947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW08944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
AAW08944
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                         epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the heavy chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RHE. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or displatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and humanised versions of anti-EGF receptor antibody 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibiting tumour growth, esp. of late stage prostatic tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 62; DB 2; Length 119; 100.0%; Pred. No. 0.0056; Pred. No. 0. 10056; Ive 0; Mismatches 0; Indels
                                                                              reshaped; monoclonal; antibody; 225RE; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saldanha JW;
                                                  Heavy chain variable region of 225RE antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Giorgio NA, Jones ST,
                                                                                                                                                                                    1. 30
/label= framework_1
31. 35
/label= CDR_1
36. 49
/label= framework_2
                                                                                                                                                                                                                                                                  50. .65
/label= CDR_2
66. .97
/label= framework_3
                                                                                                                                                                                                                                                                                                                                             109. 119 -
/label= framework_4
                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 30; Fig 22; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                   CDR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00482982
95US-00573289
                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US009847
                          (first entry)
                                                                                                                                                                                                                                                                                                                    98. .108
/label= CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100...
Local Similarity 100...
Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-051897/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goldstein NI,
                                                                             Heavy chain;
                          18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                      WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1996;
                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-1996
 AAW08954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric
                                                                                                                                                                                    Region
                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
```

- nsed

Giorgio NA, Jones ST, Saldanha JW;

96WO-US009847. 95US-00482982, 95US-00573289,

```
ö
                                                                                                                                                                                                                                                   Heavy chain, murine; mouse; monoclonal; antibody; C225; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; chimeric.
                             Gaps
                             .;
0
100.0%; Score 62; DB 2; Length 138; 100.0%; Pred. No. 0.0065; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                           Heavy chain variable region of C225 antibody
                                                                                                                                              AAW08944 standard; protein; 138 AA.
                                                                                                                                                                                                 (first entry)
            Best Local Similarity 100 Matches 11; Conservative
                                                                        117 ALTYYDYEFAY 127
                                                     1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                          Mus; spp.
Homo sapiens.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                        WO9640210-A1
                                                                                                                                                                                                 18-SEP-1997
```

ö

Gaps

. 0

RESULT 9
AAW08947
ID AAW08947 standard; protein; 138 AA.
XX

ALTYYDYEFAY 108 1 ALTYYDYBFAY 11

ò g

Gaps .. 0

```
The present sequence is the heavy chain variable region of the murine monoclonal antibody (MAD) M225, which is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to timbibt the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor. (Updated on 27-AUG-2003 to correct OS field.)
      Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single chain antibody; scFv; monoclonal antibody; MAb; EGF; epidermal growth factor; receptor; antitumour; cancer; therapy.
                                                                                                                                                                                                                                              Length 138;
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Score 62; DB 2; Length 13
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .119
/label= VH_region
/note= "monoclonal antibody 225 VH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= VL
/note= "monoclonal antibody 225 VL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "synthetic spacer peptide"
134. .240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       AAW05133 standard; protein; 240 AA.
                                                        Example IV; Fig 14; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 17; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single chain antibody scFv(225)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120. .133
/label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Groner B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95EP-00106275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                           117 ALTYYDYEFAY 127
                                                                                                                                                                                                                                                                                                             1 ALTYYDYBFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmidt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-478748/48.
N-PSDB; AAT42033.
                                                                                                                                                                                                                 Sequence 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-0CT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP739984-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus; sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW05133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wels W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                             AAW0513
                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                          The present sequence is the heavy chain variable region of the chimeric monoclonal antibody (MAD) C225, which is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heavy chain; murine; mouse; monoclonal; antibody; M225; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region.
                                                                                                                                                                                                                                                   Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 62; DB 2; Length 138; 100.0%; Pred. No. 0.0065; Pred. No. 100.08; Pred. No. 10065; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldstein NI, Giorgio NA, Jones ST, Saldanha JW;
                                                                                                                                                                         Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy chain variable region of M225 antibody.
                                                                                                                                                                           Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                   Example IV; Fig 16; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW08942 standard; protein; 138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                            (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT
                                                96WO-US009847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US009847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00482982.
                                                                                             95US-00573289
                                                                               95US-00482982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 ALTYYDYEFAY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALTYYDYBFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-051897/05.
N-PSDB; AAT49340.
                                                                                                                                                                                                       1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                        N-PSDB; AAT49343
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavy chain;
epidermal gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
15-DEC-1995;
                                                07-JUN-1996;
                                                                               07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-2003
18-SEP-1997
                   19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW08942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus
```

d

ô

Gaps

. 0

```
scFv(225) (AAW05133) comprises the single-chain binding region of murine monoclonal antibody 225, which is specific for the human epidermal growth factor receptor. It is encoded by plasmid pWW152-225 (see also AAT42033), constructed by cloning MAD 225 VH and VL region cDNAs into plasmid pWW152. Novel bivalent proteins (see also AAW05134-44), some of them including scFv(225) and an effector e.g. cytotoxin, can be produced in bacterial host cells, and are useful as antitumour agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single chain antibody, scPv; monoclonal antibody; MAb; EGF; epidermal growth factor; receptor; plasmid pSW202-225; cancer; therapy; antitumour; exotoxin A; ETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 62; DB 2; Length 240; Best Local Similarity 100.0%; Pred. No. 0.012; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290. .651
/label= ETA
/note= "exotoxin A amino acids 252-613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .21
/label= Sig_peptide
/note= "ompA signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Page 19-20; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW05135 standard; protein; 651 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SANT-) SAN TUMORFORSCHUNGS GMBH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scFv(225)-ETA fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95EP-00106275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95EP-00106275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTYYDYEFAY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
Pseudomonas, aeruginosa.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-478748/48.
N-PSDB; AAT42035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schmidt M,
                                                                                                                                                                                                                                                                 Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP739984-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wels W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW05135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
X88888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A STATE OF STATE OF STATE OF STATE OF OF STAT
```

```
ö
        scFv(225)-ETA (AAW05135) comprises the single-chain binding region (see also AAW05133) of murine moncelonal antibody 225, which is specific for human epidermal growth factor receptor, joined to exotoxin A (ETA). It is encoded by plasmid growth factor see also AAT42035) obtd. by ligating an scFv(225) gene (AAT42033) into plasmid pSW200 contg. the Pseudomonas acruginosa PAK ETA gene. The construct can be used to produce novel bivalent fusion proteins (see also AAW05136-44) in bacterial host cells, for use as antitumour agents
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                           Single chain antibody; scFv; monoclonal antibody; NAb; EGF; erbB-2; epidermal growth factor; receptor; plasmid pMS238-225-5; cancer; exotoxin A; ETA; antitumour.
                                                                                                                                                              ..
0
                                                                                                                                    100.0%; Score 62; DB 2; Length 651;
100.0%; Pred. No. 0.036;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               648. .658
/label= Spacer
659. .892
/label= ETA
/note= "endotoxin-A amino acids 380-613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290. .404
|label= ETA
|note= "exotoxin A amino acids 252-366"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . . 21
/label= Sig peptide
/mote= "ompA signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                 AAW05140 standard; protein; 892 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22. .38
/label= Spacer
39. .279
/label= scFv(225)
279. .289
/label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCFV (FRP5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spacer 647 /label= sr. 748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95EP-00106275
                                                                                                                                                                                                                                                                                                               29-JAN-1997 (first entry)
                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                      136 ALTYYDYEFAY 146
                                                                                                                                                                                    1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                          Mus; sp.
Pseudomonas; aeruginosa.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                    scrv2 (225/FRP5) -ETA.
                                                                                                               Sequence 651 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-OCT-1996.
                                                                                                                                                                                                                                                                                       AAW05140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                          RESULT 14
AAW05140
X8888888888XX
                                                                                                                                                                                    à
                                                                                                                                                                                                        임
```

```
WPI; 1996-478748/48.
                                                                                                                                                                                                                                                                                          N-PSDB; AAT42039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 892 AA;
                                                                                                     26-APR-1995;
                                                                                                                                             26-APR-1995;
                   EP739984-A1.
                                                           30-0CT-1996.
                                                                                                                                                                                                                            Wels W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search comp
Job time :
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                      scFv2(225/FRP5)-ETA (AAW05140) comprises the single-chain binding region of murine monoclonal antibody 225 (specific for human epidermal growth factor receptor, see also AAW0513) Joined to portions of exocorin A from Pseudomonas aeruginosa and to the single-chain binding region of murine monoclonal antibody FRP5 (specific for human epidermal growth factor receptor exbB-2, see also AAW05134). It is encoded by plasmid pMS238-225-5 (AAT42040). This plasmid can be utilised in the prodn. of the bivalent fusion protein in bacterial (sep. B. coli) host cells. Such fusion proteins (see also AAW05138-44) are useful as antitumour agents
                                                                                                   Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single chain antibody; scFv; monoclonal antibody; MAb; EGF; erbB-2;
epidermal growth factor; receptor; plasmid pMS238-5-225; cancer;
exotoxin A; ETA; antitumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 62; DB 2; Length 892; 100.0%; Pred. No. 0.051; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "endotoxin-A amino acids 380-613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "exotoxin A amino acids 252-366"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ....21
/label= Sig peptide
/note= "ompA signal peptide"
                                                                                                                                                                                       Example 11; Page 31-33; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279. .289
/label= Sr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW05139 standard; protein; 892 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scFv (225)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scFv2(FRP5/225)-ETA (version 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22. .38
/label= Spacer
39. .278
/label= scFv(FR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                648. .658
/label= Spacer
659. .892
/label= ETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spacer
    Groner B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290. .404
/label= ETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       707
/label= Sr
78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .647
/label= e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 ALTYYDYEFAY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas; aeruginosa.
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALTYYDYEFAY 11
                                         WPI; 1996-478748/48.
N-PSDB; AAT42040.
  Schmidt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 892 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW05139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAWO5139
LD AAWO51
    d
```

```
ocFv2(FRP5/225)-ETA (AAW05139) comprises the single-chain binding region of murine monoclonal antibody FRP5 (specific for human epidermal growth factor receptor erbB-2, see also AAW05134) joined to portions of exotoxin A from Pseudomonas aeruginosa and to the single-chain binding region of murine monoclonal antibody 225 (specific for human epidermal growth factor receptor, see also AAW05133). It is encoded by plasmid pMS228-5-225 (AAT42039). This plasmid can be utilised in the prodn. of the bivalent fusion protein in bacterial (sep. E. coli) nost cells. Such fusion proteins (see also AAW05138-44) are useful as antitumour agents
                                                                                                                                                                                                                                                                                                                                                                                                          Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 62; DB 2; Length 892;
100.0%; Pred. No. 0.051;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         completed: October 6, 2004, 16:29:45
Ne : 57.5789 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 11; Page 28-30; 52pp; English.
                                                                                                                                                SANT-) SAN TUMORFORSCHUNGS GMBH.
95EP-00106275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 100.
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALTYYDYEFAY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505 ALTYYDYEFAY
                                                                                                                                                                                                                             Schmidt M,
```

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

007 TO:/80 PT 000 TI

OM protein - protein search, using sw model

October 6, 2004, 16:34:15 ; Search time 68.5088 Seconds (without alignments) 51.669 Million cell updates/sec

Run on:

US-09-635-974A-8 55 Title: Perfect score:

1. RASQSIGTNIH 11 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1351062 seqs, 321799191 residues Searched:

1351062 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:\*

1: \cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
2: \cgn2\_6/ptodata/2/pubpaa/PCT\_MBW PUBL.pep:\*
3: \cgn2\_6/ptodata/2/pubpaa/PCT\_MBW PUBL.pep:\*
4: \cgn2\_6/ptodata/2/pubpaa/US06\_NEW PUBL.pep:\*
5: \cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
6: \cgn2\_6/ptodata/2/pubpaa/US07\_NEW PUB.pep:\*
7: \cgn2\_6/ptodata/2/pubpaa/US08\_NEW PUB.pep:\*
8: \cgn2\_6/ptodata/2/pubpaa/US08\_NEW PUB.pep:\*
9: \cgn2\_6/ptodata/2/pubpaa/US08\_NEW PUB.pep:\*
11: \cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
11: \cgn2\_6/ptodata/2/pubpaa/US09E\_PUBCOMB.pep:\*
11: \cgn2\_6/ptodata/2/pubpaa/US09E\_PUBCOMB.pep:\*
13: \cgn2\_6/ptodata/2/pubpaa/US09E\_PUBCOMB.pep:\*
14: \cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
15: \cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
16: \cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
17: \cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
18: \cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
17: \cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
18: \cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
18: \cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |    | Description |        | Sequence 32, Appl | Sequence 8, Appli | Sequence 100, App | Sequence 100, App | Sequence 25, Appl | Sequence 113, App | Sequence 114, App | Sequence 113, App | Sequence 114, App | Sequence 129, App  | Sequence 5, Appli | Sequence 11, Appl | Sequence 15, Appl | Sequence 17, Appl | Sequence 5, Appli |
|-----------|----|-------------|--------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| COMMAKIBO |    | Ę           |        | US-09-798-689-32  | US-09-996-954B-8  | US-10-374-600-100 | US-10-374-531-100 | US-09-991-470-25  | US-10-374-600-113 | US-10-374-600-114 | US-10-374-531-113 | US-10-374-531-114 | US-10-412-703A-129 | US-10-374-600-5   | US-10-374-600-11  | US-10-374-600-15  | US-10-374-600-17  | US-10-374-531-5   |
|           |    |             | !      | 10                | 10                | 12                | 15                | σ                 | 12                | 12                | 15                | 15                | 15                 | 12                | 12                | 12                | 12                | 12                |
| de        |    | Query       | 110000 | 11                | 11                | 11                | 11                | 107               | 107               | 107               | 107               | 107               | 108                | 127               | 127               | 127               | 127               | 127               |
|           | dю | Query       |        | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 100.0              | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             |
|           |    | Q.          |        | 55                | 55                | 55                | 52                | 55                | 55                | 55                | 55                | 55                | 55                 | 52                | 52                | 55                | 53                | 55                |
|           |    | Result      | 2 1    | 1                 | 7                 | e                 | 4                 | Ŋ                 | 9                 | 7                 | 8                 | o,                | 10                 | 11                | 12                | 13                | 14                | 15                |

| Sequence 11, Appl<br>Sequence 15, Appl<br>Sequence 27, Appl<br>Sequence 27, Appl<br>Sequence 27, Appl<br>Sequence 27, Appl<br>Sequence 27, Appl<br>Sequence 129, Appl<br>Sequence 129, Appl<br>Sequence 130, Appl<br>Sequence 130, Appl<br>Sequence 130, Appl<br>Sequence 130, Appl<br>Sequence 130, Appl<br>Sequence 13, Appli<br>Sequence 17, Appli<br>Sequence 17, Appli<br>Sequence 28, Appli<br>Sequence 28, Appli<br>Sequence 28, Appli<br>Sequence 28, Appli<br>Sequence 28, Appli<br>Sequence 28, Appli<br>Sequence 1, Appli<br>Sequence 30, Appli<br>Sequence 30, Appli<br>Sequence 30, Appli |  |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
| 15 US-10-374-531-11<br>16 US-10-374-531-15<br>17 US-09-991-470-27<br>18 US-09-991-470-27<br>19 US-10-239-656-39<br>10 US-10-239-656-39<br>10 US-10-308-817-27<br>12 US-10-308-817-129<br>12 US-10-308-817-129<br>13 US-10-339-656-38<br>14 US-10-339-656-38<br>15 US-10-339-656-38<br>16 US-10-339-656-29<br>17 US-10-339-656-29<br>18 US-09-956-206-37<br>19 US-10-339-656-29<br>10 US-10-339-656-29<br>11 US-10-339-656-29<br>12 US-10-339-656-29<br>13 US-10-339-656-29<br>14 US-10-339-656-29<br>15 US-10-339-656-29<br>17 US-10-339-656-29<br>18 US-10-339-656-29<br>19 US-10-339-656-29<br>10 US-10-336-210-8<br>11 US-10-339-656-28<br>12 US-10-339-656-28<br>13 US-10-336-210-8<br>14 US-10-336-210-8<br>15 US-10-336-210-8<br>16 US-10-443-466A-8<br>17 US-10-453-698-38<br>18 US-10-656-769-71<br>19 US-10-656-769-71                                                                                                                        |  |
| 1127<br>245<br>245<br>245<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |  |
| 1111<br>000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |  |
| N N N N N N N N N N N N N N A 4 4 4 4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |  |
| 11111222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |  |

## ALIGNMENTS

RESULT 1
US-09-798-689-32
i Sequence 32, Application US/09798689
i Publication No. USZ0030103973A1
i General No. USZ0030103973A1
i APPLICANT: Rockwell, Patricia
APPLICANT: Rockwell, Patricia
APPLICANT: Gendatein, Method for Reducing Tumor Growth with VEGF Antagonists
TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REPERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: 09/09/798, 689
CURRENT FILING DATE: 2001-03-02
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR PELING DATE: 1996-09-03
PRIOR PELING DATE: 1996-09-03
PRIOR PELING DATE: 1996-09-03
PRIOR PELING DATE: 1996-09-03
PRIOR PILING DATE: 1996-09-03
PRIOR PILING DATE: 1996-09-03
PRIOR PELING DATE: 1996-09-03
PRIOR PILING DATE: 1996-09-03
PRIOR PILING DATE: 1996-00-03
PRIOR PELING DATE: 1996-00-0 Gaps ; 0 Length 11; Indels Query Match 100.0%; Score 55; DB 10; Best Local Similarity 100.0%; Pred. No. 0.00059; Matches 11; Conservative 0; Mismatches 0; ; ORGANISM: Mouse US-09-798-689-32

1 RASQSIGTNIH 11

ö

à

Gaps

g

```
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-10-374-531-100
; Sequence 100, Application US/10374531
; Publication No. US20040006212A1
; GENERAL INFORMATION:
APPLICANT: ImClone Systems Incorporated, et al.
; APPLICANT: ImClone Systems Incorporated, et al.
ITILE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INFIER OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 55, DB 12;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 11; Conservative 0; Mismatches 0;
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-E6b-2003
CLASSIFCATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                        (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: (212) 425-7200 (212) 425-5288
                                                                                                425-5288
                                                                   TELEPHONE: (212) 425-72
TELEFAX: (212) 425-528
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                       Sequence 8, Application US/0996954B

Publication No. US20030157104A1

GENERAL INFORMATION:

APPLICANT: Waksal, Harlan W.

TITLE OF INVENTION: Treatment of Refractory Human Tumors

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists

TITLE OF INVENTION: WITHER: US/09/996,954B

CURRENT FILING DATE: 2001-11-30

FRIOR PILING DATE: 04-24-2001

FRIOR APPLICATION NUMBER: 09/374,028

FRIOR FILING DATE: 08-13-1999

PRIOR FILING DATE: 05-14-1999

NUMBER OF SEQ ID NOS: 12

SEQ ID NOS: 12

SEQ ID NOS: 12

SEQ ID NOS: 12

SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-10-374-600-100
; Sequence 100, Application US/10374600
; Publication No. US20030224001A1
; Publication No. US20030224001A1
; GENERAL INFORMATION:
; APPLICANT: ImClone Systems Incorporated, et al.
; TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRACMENTS FOR TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 55; DB 10; Length 11; 100.0%; Pred. No. 0.00059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/10/374,600
FILING DATE: 22-F6-2003
CLASSIFICATION - CURLOWN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1996
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens-Rodent Chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RASQSIGTNIH 11
  1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RASOSIGINIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΩS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                JS-09-996-954B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-996-954B-8
```

ઠે 임

```
1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-374-600-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-374-600-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application US/09991470

Sequence 25, Application US/09991470

Patent No. US20020173477A1

GENERAL INFORMATION:

APPLICANT: Ruey S. Liou

TITLE OF INVENTION: ANTI-IGE GENE THERAPY

FILE REFRENCE: 99-2

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/397,569

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 25

LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 113, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 9; Length 107; 100.0%; Pred. No. 0.0065; Live 0; Mismatches 0; Indels
                                                                                                                                     Length 11;
                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: 1000 occupantible
COMPUTER: 1EM compatible
COMPUTER: 1EM compatible
COMPUTER: 05-75TM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION UNMER: 03/10/374,600
FILING DATE: 25-Feb-2003
CLASSIPICATION: cUnknown>
                                                                                                                                   Query Match 100.0%; Score 55; DB 15; Best Local Similarity 100.0%; Pred. No. 0.00059; Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-374-531-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RASQSIGINIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RASOSIGTNIH 11
                                                                                                                                                                                                                                                              1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: human/murine
US-09-991-470-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-374-600-113
                                                                                                                                                                                                                                                                                                                                                 JS-09-991-470-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                              g
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 114, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
AITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INVENTION: INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect COMPUTER: Wordperfect CURRENT APPLICATION NUMBER: US/10/374,600

FILING DATE: 25-Feb-2003

CLASSIFICATION CURNOWN>
PRIOR APPLICATION NUMBER: US/08/973,065C

FILING DATE: 19-Mar-1998

APPLICATION NUMBER: PCT/US96/0987

FILING DATE: 07-JUN-1996

APPLICATION NUMBER: US 08/482,992

FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
FILING DATE: 07-JUN-1996

APPLICATION NUMBER: US 08/82,982
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
FILING DATE: 15-DEC-1995
FILING DATE: 15-DEC-1995
ATORNEY/AGENT INFORMATION:
NAME: DEDOTAR A. SOMETVILLE
REGISTRATION NUMBER: 31,995
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELEPHONE: (212) 425-7200
TELEPHONE: (212) 425-588
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acid
STRANDENESS: not relevant
TOPOLLOGY: not relevant
TOPOLLOGY: NO relevant
SEQUENCET TYPE: Epptide
HYPOTHETICAL: NO
FRAGNENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 55; DB 12;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
```

à

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                              SSULT 9
$-10-374-531-114
Sequence 114, Application US/10374531
Publication No. US20040006212A1

GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
IITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INFIBITING THE GROWTH OF TUMORS
                                                       100.0%; Score 55; DB 15; Length 107; 100.0%; Pred. No. 0.0065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 55; DB 15; Length 107; 100.0%; Pred. No. 0.0065; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION: <u v curronna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 114: US-10-374-531-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
STREET: One Broadway
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 114: SEQUENCE CHARACTERISTICS:
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
                                                                                                                                               1 RASQSIGTNIH 11
                                                                                                                                                                                           24 RASOSIGINIH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RASQSIGTNIH 11
                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserv
           US-10-374-531-113
                                                                                                  11;
                                                                                                  Matches
                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-10-374-531-113
Squence'113, Application US/10374531
Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: InClone Systems Incorporated, et al.
TILE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR
                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 12; Length 107; 100.0%; Pred. No. 0.0065;
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIORIGATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-MAT-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/ACBNT INFORMATION:
NAME: Deborate A. Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acide
TYPE: amino acid
STRANDEDNESS: not relevant
POPOLOGY: not relevant
HYPOTHETICAL: NO
FRAGMENT TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-374-600-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           1 RASOSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                      24 RASOSIGTNIH 34
```

. 0

Gaps

.; 0

```
NS-10-374-600-11

Sequence 11, Application US/10374600

Publication No. US20030224001A1

Publication No. US20030224001A1

Publication No. US2003024001A1

INTILE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR NUMBER OF SEQUENCES: 120

CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CIT: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NAVER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                 100.0%; Score 55; DB 12; 100.0%; Pred. No. 0.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 425-7200
TELEFRAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1996
APPLICATION NUMBER: US/08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-10-374-600-11
                                                                                                                                                                     FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-10-374-600-5
                                                                  STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                          1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                      Sequence 129, Application US/10412703A

Publication No. US20030219439A1

GENERAL INFORMATION:

APPLICANT: Reed et al.

TITLE OF INVENTION: Recombinant Anti-Interleukin-9 Antibodies

FILE REFERENCE: 114000BC

CURRENT FILING DATE: 2003-04-11

PRIOR APPLICATION NUMBER: 60/371,728

PRIOR FILING DATE: 2002-04-12

SEQ ID NOS: 140

SOFTWARE: Patentin version 3.2

LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 55; DB 15; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10374600
Publication No. US20030224001A1
GENERAL INPORMATION:
APPLICANT:/IMClone Systems Incorporated, et al.
TITLE OF INVENTION: INFIBODY AND ANTIBODY FRAGMENTS FOR INFIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: US

ZIP: 10004

COUNDUTER: New YOLK

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMFIGNATION SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,600

FILING DATE: 25-Feb-2003

CLASSIFICATION: CURNOWN>
PRIOR APPLICATION NUMBER: US/08/973,065C

FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847

FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 10-Mar-1998
APPLICATION NUMBER: US 08/482,982
FILING DATE: 10-JUN-1996
APPLICATION NUMBER: US 08/573,289
APPLICATION NUMBER: US 08/573,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RASOSIGINIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
US-10-412-703A-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
```

```
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                       STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SIE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-374-531-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
 Length 127;
                                                                                                                                                                                                                            DDICATION NO.
GENERAL INFORMATION:
APPLICANT: IMCIONE Systems Incorporated, et al
APPLICANT: IMCIONE SYSTEMS INCORPORTED OF TITLE OF INVENTION: INHIBITING THE GROWTH OF TUMORS
INHIBITING THE GROWTH OF TUMORS
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 100.0%; Score 55; DB 12; Similarity 100.0%; Pred. No. 0.0079; 11; Conservative 0; Mismatches 0;
Query Match 100.0%; Score 55; DB 12; Best Local Similarity 100.0%; Pred. No. 0.0079; Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/573,289
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REPERBNCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 15: US-10-374-600-15
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212) 425-7200
                                                                                                                                                               RESULT 13'
US-10-374-600-15
Sequence 15, Application US/10374600
Publication No. US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                        1 RASOSIGINIH 11
                                                                                                              44 RASOSIGTNIH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 RASOSIGTNIH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 11; Conservat
                                                                          à
```

RESULT 14 US-10-374-600-17

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indela
Sequence 17, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
APPLICANT: Imclone Systems Incorporatedy et al.
ITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS
TITLE OF INVENTION: INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                       ZIP: 10004 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 12; 100.0%; Pred. No. 0.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION UNWER: US/08/973,065C
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC_1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRACMENT TYPE: internal
;
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-374-600-17
                                                                                                                                                           CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSES
STREET: Come Broadway
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
CORRESPECT: Kenyon & Kenyon
SIREET: One Broadway
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 127 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/10374531
; Publication No. US20040006212A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
```

```
STATE: New York

COUNTRY RADABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage

COMPUTER: IBM compatible

OMPUTER: IBM compatible

FILING DATE: 15-P6-2003

APPLICATION NUMBER: US/08/973,065C

FILING DATE: 15-DEC-1996

APPLICATION NUMBER: US 08/42/982

ATTONNEY/AGRIT INFORMATION:

NAME: Deborah A. Somerville

AMPLICATION NUMBER: 11245/46003

FILING DATE: 15-DEC-1995

ATTONNEY/AGRIT INFORMATION:

IMPORMATION INFORMATION:

SEQUENCE (12) 425-7200

TELEBCAMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

SEQUENCE (12) 425-7200

TELEBCAM SEQ ID NO: 5:

LENGTH: 127 amino acide

TYPE: infernal

SEQUENCE TREES: peptide

HYPOTHETION: NEW INFORMATION:

MOLECULE TYPE: infernal

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

DEPART TYPE: infernal

SEQUENCE DESCRIPTION: SEQ ID NO: 0.0079;

TOPLOGY: DESCRIPTION: 0.0079;

TO
```

Search completed: October 6, 2004, 17:09:05 Job time : 70.5088 secs

44 RASQSIGTNIH 54

ô

0; Gaps

Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 11; Conservative 0; Mismatches 0; Indels C

This Page Blank (uspto)

0.

Title: Perfect score: Sequence: Scoring table:

Searched:

Database :

OM protein

Run on:

```
QVIIB3 homo sapien
QVIIB3 homo sapien
QVIIB2 pyrcoccus
QVIID2 pyrcoccus
QVIID2 pyrcoccus
QVIID3 pyray
QVIID3 wis musculu
QVIID3 aspergillus
QWIA3 aspergillu
Q7w642 bordetella
Q7vvm0 bordetella
Q93yg8 lycopersico
065833 lycopersico
Q7ux08 rhodopirell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OBmwwl scarites su
Q8mx00 dicaelus am
Q88st3 lactobacill
Q98mj2 rhizobium l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.2%; Score 43; DB 11; Length 127; 72.7%; Pred. No. 0.9; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q925S9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seque:
01-OCT-2003 (TrEMBLrel. 25, Last annot:
Immunoglobulin light chain (Fragment).
Mus musculus (Mouse).
0774642
0937CW0
0937CW0
065833
065833
097UX08
097UHZ
0897UHZ
0897UHZ
0897HZ
0897HZ
0897HZ
0817HZ
081
                                                                                                                                                                Query Match
Best Local Similarity 72.",
Best Local Similarity 72.",
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||| || |:|
44 RASQDIGINLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       092589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
Q925S9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDD REPARED DESTROY OF THE PROPERTY OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ୍ଦର
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q92599 mus musculu Q8vij0 mus musculu Q8vij0 mus musculu Q8ub65 homo sapien Q8ucalu pyrococcus Q8btu3 mus musculu Q8btu3 caenorhabdi Q7yxu6 caenorhabdi Q5pa89 xanthomonas Q8ukj0 agrobacceri Q9azb3 lactobacill Q8G05 methanosarc Q33542 clivia mini Q9Em99 tribolium c Q7wi08 bordetella
                                                                                                                                                                                  October 6, 2004, 16:23:13; Search time 36.8596 Seconds (without alignments) 94.160 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         092589
08010
08010
080103
080803
080803
096508
078706
078706
097809
09783
09789
09789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPTREMBL_25:*

1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_human:*
5: Sp_invertebrate:*
6: Sp_mammal:*
7: Sp_mhc:*
8: Sp_organelle:*
9: Sp_phage:*
10: Sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_archeap:*
                                                                                                                                                                                                                                                                                                 US-09-635-974A-8
55
1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
1132
1332
1332
1336
1442
1442
11334
11334
11334
11334
11334
```

Score

Result

ô

```
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22579291; PubMed=12693553;
Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
Nakajima D., Nagase T., Ohara O., Koga H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1186 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                               Putative ribose ABC transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKIAA0684 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.3%;
Pfam; PF00607; Gag p24; 1.
Pfam; PF00098; zf-CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                || | : || : |
97 RACQDVGTELH 107
                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 RABEAMGVNVH 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                               1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKIAA0684.
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                              PF1698.
                                                                                                                                                                                                                                                             Q8U0A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q80TU3
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
Q80TU3
                                                                                                                                                                                                                                  RESULT 4
                                                                                                                                                                                                                                               Q8U0A1
                                                                                                                                                                                                                                                               임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                     STRAIN=C3H/HeJ-lpr/lpr;
MEDLINE=96409289; PubMed=8814271;
Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
"Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
Eur. J. Immunol. 26:2225-2233(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., Ishidashi T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Takahashi-Fuji A., Oshima A., Sugiyama A., Kawakani B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 11; Length 108;
Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "NEDO human CDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AK091495; BAC03676.1;
GO; GO:0003676; P:nucleic acid binding; IEA.
GO; GO:0016032; P:viral life cycle; IEA.
InterPro; IPR000721; Gag_p24.
InterPro; IPR000721; Gag_p24.
InterPro; IPR001816; Retrov capsid_C.
                                                                                                                                                                                                                                                                                                                                                                                                                             108 AA; 11859 MW; 68506D75613DBFBE CRC64;
                                                        Q8VIJO;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ34176.
Homo sapiens (Human).
                                          108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                          PRT;
                                                                                                           Anti-DNA light chain (Fragment).
                                                                                                                                                                                                                                                                                                   EMBL; U59155; AAB02917.1; -...
PIR; A33933; A33933.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PP00047; ig; 1...
SWART; SW00406; IGv; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 60.0 es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                   108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RASQSIGTNI 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 KASQNVGTNV 33
                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                 108
                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08NB65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8NB65
                                          QBVIJO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
              RESULT 3
Q8NB65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrococcus furiosus.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=VC1 / DSM 3338 / ATCC 43587 / JCM 8422;
STRAIN=VC1 / DSM 3338 / ATCC 43587 / JCM 8422;
STRAIN=VC1 / DSM 3338 / BTCC 43587 / JCM 8422;
STRAIN=VC1 / DSM 3338 / BTCC 43587 / JCM 8422;
The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ABC10267; AAL61822.1;
GO, GO:00160205; Fitransporter activity; IEA.
GO, GO:0006810; Pitransport: IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 17; Length 302;
Pred. No. 40;
5; Mismatches 1; Indels
                                                                                                                                                                       67.3%; Score 37; DB 4; Length 212; 54.5%; Pred. No. 27;
                                                                                                                                                                                                                                Indels
PRINTS; PR00939; C2HCZNFINGER.
SMART; SN00343; ZnF C2HC; 1.
PR0STTE; PS50158; ZF CCHC; 1.
Hypotherical protein.
SEQUENCE 212 AA; 23378 MW; 2070DE43BD5EE228 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001851; Bac_inmem_transp.
Pfam, PF02653; BPD transp_2; Complete processes Hypotheral protein.
SEQUENCE 302 AA; 32345 NW; DDE3122589EBSBEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 AA
                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
```

70

```
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                 Q965V8;
01-DEC-2001
                                                                                                                                                                     Y43B11AL.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y43B11AL.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7YXU6
                             Q965V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
Q7YXU6
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
"Prediction of the coding sequences of mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";

DNA Res. 10:35-48(2003).

EMBL; AK122345; BAC65627.1; -.

InterPro; IPR003613; Znf modRING.

Pfam; PFC4564; U-box; 1.

SMART; SM00504; Ubox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Xim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blutt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.,
"Oryza sativa chromosome 10 BAC OSJNBAO062C05 genomic sequence.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enthartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
The Rice Chromosome 10 Sequencing Consortium;
In-depth view of structure, activity, and evolution of rice chromosome 10.";
                                                                                                                                                                                                                                                                                 Length 1186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.5%; Score 36; DB 10; Length 132; 85.7%; Pred; No. 25; 0; Indels tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               67.3%; Score 37; DB 11; Length 11
66.7%; Pred. No. 1.8e+02;
cive 2; Mismatches 1; Indels
                                                                                                                                                                                                               NON_TER 1 1
SEQÜENCE 1186 AA; 134813 MW; 2FC25DC03820A175 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Nipponbare,
Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q
Submitted (MAX-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AC084023, AAN05573.1; -.
EMBL, AE017110; AAP54223.1; -.
Hypochetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Wypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 300:1566-1569(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                        |||:| |:|
SQSLGLNVH 71
                                                                                                                                                                                                                                                                                                                                                                               3 SOSIGINIH 11
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
6, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 SIGTNVH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 SIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=39947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8H8X2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8H8X2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08H8X2
    RATTAL
DRING
STANDAR
DRING
STANDAR
STA
                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                         임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .; IEA.
                                                                                                                                                         Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
"Direct Submission.";
Submitted (JUN-2001). to the EMBL/GenBank/DDBJ databases.
BMBL; AC02479; AAK68485.1;
"NormPep; Y43B11AL.2; CE28564.
GO; GO:0001584; F:inhedgral to membrane; IEA.
GO; GO:0001584; F:inhedgral to membrane; IEA.
GO; GO:0001586; P:inhedgral to membrane; IEA.
HILLEPPO; IPROGONZ6; GPCR Rhodgen.
INTERPO; JRR0000276; GPCR Rhodgen.
RNOSTIF: SS50262; G PROTEIN RECEP F1 2; 1.
SEQUENCE 299 AA; 34315 NW; 11G371C5C63A4D70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cordes M., Maupin R.;
"The sequence of C. elegans cosmid Y43B11AL.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Y43B11AL.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.5%; Score 36; DB 5;
80.0%; Pred. No. 63;
live 0; Mismatches
299 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
PRT;
                                                                                                                                                                                                                                                                             STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 ASQSIGDAIH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
```

```
Query Match
Best Local Similarity
                                                                                                                                                                                            Complete proteome
SEQUENCE 428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08UKJ0
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8UKJ0
ò
                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
MEDLINE=22022145; PubMed=12024217;
Malline=22022145; PubMed=12024217;
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
Formighieri B.F., Franco M.C., Graggio C.C., Gruber A.,
Formighieri B.F., Franco M.C., Graggio C.C., Gruber A.,
Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.5%; Score 36; DB 5; Length 304;
80.0%; Pred. No. 64;
tive 0; Mismatches 2; Indels
                 Cordes M., Maupin R.; "The sequence of C. elegans cosmid Y43B11AL."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                        [3]
SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Waterston R.H.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC024779; AAP86615.1; -.
                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
Waterston R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 304 AA; 34724 MW; 7F7F6C54C4F69589 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 ASOSIGDAIH 45
                                                                                                                                                                                                                                                          Submitted (JUN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.,
Submitted (NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=Bristol N2; Waterston R.;
                                                                                                                                                                                                                                                                                 [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Bristol N2;
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydroxylase,
MBTG OR XCC1598,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBPA89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8PA89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 PA 89 PA 
d
```

```
.;
0
Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
Sprinla L.M., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
Trindade dos Sancos M., Truffi D., Tsai S.M., White F.F.,
Setubal J.C., Kitajima J.P.;
Comparison of the genomes of two Xanthomonas pathogens with differing
Not specificities.";
Nature 417:459-463(2002).
EMBL, ABM10892.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-2160551; PubMed=11743194; Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILNE=21608550; PubMed=11743193; MeDILNE=21608550; PubMed=11743193; MeDILNE=21608550; PubMed=11743193; Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Wood L.W., Zhou Y., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Rutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence" of the plant pathogen and biotechnology agent Agrobacterium tumefaciens CS8."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 16; Length 428;
Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                          428 AA; 47012 MW; FA7C59345838FFE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; AD3173; AD3173.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
Hypothetical protein; Plasmid; Complete proteome.
SEQUENCE 440 AA; 48826 WW; 583770DD1576D6F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agrobacterium Tumefaciens (strain C58 / ATCC 33970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBUKJO;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atuši12.
ATUSI12 OR AGR_PAT_166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE008936; AAL45802.1; -. EMBL; AE007884; AAK90488.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RASOSICTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || | || :||
75 RARQKIGVSIH 85
```

65.5%; Score 36; DB 16; Length 440; 54.5%; Pred. No. 97;

ò d 

```
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Asparagales, Amaryllidaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gonzalez J.M., Robb F.T.;

Gonzalez J.M., Robb F.T.;

"A genomic survey of the extreme thermophilic, CO-utilizing bacterium carboxydochemus bydrogenoformans.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF244604; AAG23553.1; -.

GO; GO:0016740; Fitransferase activity; IEA.

GO; GO:0016740; Fitransferase activity; IEA.

GO; GO:0016740; Fitransferase activity.

InterPro; IPR003702; ActCoA hydro.

Pfam; PF02550; AcetylCoA hydro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Damme E.J., Smeets K., Van Leuven F., Peumans W.J.;
"Molecular cloning of mannose-binding lectins from Clivia miniata.";
Plant Mol. Biol. 24:825-930(1994).

EMBL, L16512; AAA19911.1;
PIK, 843762, 843762.

GO, GO:0005529; F:sugar binding; IEA.

InterPro: IRF001480; B_lectin.

Pfam, PF01453; Agglutini; 1.

SMART; SM00108; B_lectin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carboxydothermus hydrogenoformans.
Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 10; Length 169;
Pred. No. 53;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LECTIN.
855FD8A3FF7F0B5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 211
211 AA; 23149 MW; C3038601E0C79E82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
4-hydroxybutyrate CoA transferase (Fragment).
                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94250846; PubMed=8193308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 AA; 18138 MW;
                                                                                                                                                                                                                              (TrEMBLrel. 01, C
(TrEMBLrel. 01, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.6%;
70.0%;
                                                                                                                                                                                                                                                                                                                                         Lectin precursor (Fragment)
Clivia miniata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 70.(
   KGSDSIGRNLH 100
                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASWATGTNIH 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ASOSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=129958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=16049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carboxydothermus
                                                                                                                                                                  Q39542
Q39542;
01-NOV-1996
                                                                                                                                                                                                                                                                     01-NOV-1996
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130
   90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clivia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9F8M9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9F8M9
                                                                                                      RESULT 13
Q39542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9F8M9
                                                                                                                                                                         STTTT THE SOLUTION OF THE SOLU
   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SO PER REPRESENTATION OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
STRAIN=22120827; PubMed=12125824;
MEDLINE=22120827; PubMed=12125824;
Deppermeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Brueggemann H., Likhdis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
Fritz H.-J., Gottschalk G.,
"The genome of Methanosarcina mazei: evidence for lateral gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20455575; PubMed=10998330;
Desiere F., Pridmore R.D., Brussow H.;
"Comparative genomics of the late gene cluster from lactobacillus
   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanosarcina mazei (Methanosarcina frisia).
Archhaes, Buryarchaeota; Buryarchaeota orders incertae sedis;
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
NCBI_TaxID=2209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.5%; Score 36; DB 9; Length 1434; 66.7%; Pred. No. 3.6e+02; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.6%; Score 35; DB 17; Length 139; 54.5%; Pred. No. 43; 3; Indels Live 2; Mismatches 3; Indels
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virology 275:294-305(2000).
EMBL, AF195900, AAK27908.1; -.
SEQUENCE 1434 AA; 158446 MW; 0EB8B5A863BC4C2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transfer between Bacteria and Archaea.";
J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
EMBL, ABO13243, AAM2988.1;
Hypotherical protein; Complete proteome.
SEQUENCE 139 AA; 16170 MW; 28AF39CBEFCD9752 CRC64;
                                                                                                                                                                                                                                                                                                                              Q9AZB3;
01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2002 (TrEMBLrel. 22, Last annotation update)
Putative minor tail protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
   ٠,
ښ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 AA.
                                                                                                                                                                                                                                                                                                     PRT; 1434 AA.
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactobacillus johnsonii prophage Lj965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2002 (TrEMBLrel, 22, 01-0CT-2002 (TrEMBLrel, 22, 01-0CT-2002 (TrEMBLrel, 22, Hypothetical protein MM0192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.5.
Best Local Similarity 64.5.
   6; Conservative
                                                                                                                               RIAQEIGLNVH 239
                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                               1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|:||:||:
1339 AQNIGSNIH 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=139870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8Q0E5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORF1434
                                                                                                                                                                                                                                                                                                  09AZB3
                                                                                                                                                                                                                                  RESULT 11
Q9AZB3
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
Q8Q0E5
```

8 g ò

.. 0

Gaps

.; 0

```
ö
                                                                                                         ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.;
In Nature 0:0-0(2002).
In Substitution Incortion Nuclear (BY SIMILARITY).

EMBL; AY074761; AAL71874.1; -..

BMC; G000003700; F:transcription of transcription, DNA-dependent; IEA.

G0; G0:0003700; F:transcription of transcription, DNA-dependent; IEA.

G0; G0:000535; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPRO0182; Antennapedia.

PRO05: Probom; PRO0005; ANTENNAPEDIA.

PRODCH; SMOROS; ANTENNAPEDIA.

PROSTIE; PS00022; ANTENNAPEDIA; 1.

PROSTIE; PS00027; HOMEOBOX; 1.

PROSTIE; PS00011; HOMEOBOX; NUCLEAR PROFESSION; HOMEOBOX; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tribolium castaneum (Red flour beetle).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopteray Caleoptera, Coleoptera, Polyphaga, Cucujiformia, Tenebrionidae, Tribolium.
NCBI_TaxID=7070;
Query Match 63.6%; Score 35; DB 2; Length 211; Best Local Similarity 70.0%; Pred. No. 68; Mismatches 1; Indels Matches 7; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 63.6%; Score 35; DB 5; Length 314; Best Local Similarity 60.0%; Pred. No. 1.18+02; Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Ultrabithorax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                        183 ASESIGTKIY 192
                                                                                                                                                                                                              2 ASOSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
Q8T939
ID Q8T939
```

Search completed: October 6, 2004, 16:33:57 Job time: 41.8596 secs

:|| :||: 189 SSQPVGTQIH 198

2 ASQSIGTNIH 11

상 임

```
Pol642 mus musculu Q9es00 mus musculu Q9es00 mus musculu Q9es00 mus musculu Q9s155 homo sapien Q92g15 rickettsia Pol310 homo sapien Pol6311 homo sapien Pol6311 homo sapien Pol6312 homo sapien Pol632 arabidopsis Q9ng26 lactococcus Pol200 herpes simp Q9cg26 lactococcus Pol200 herpes simp Q9cg26 lactococcus Pol307 mus musculu Pol200 herpes simp Q9cg26 lactococcus Pol307 arabidomonas Q07938 saccharomyc Q58466 methanococc Q9pn47 anabaena sp Q46837 escherichia Q9yg22 acropyrum p P41396 actinobacil P7309 escherichia Q4100 pseudomonas Pol4013 human papil P43010 haemophilus P5543 solanum tub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                        6, 2004, 16:21:13 ; Search time 6.75439 Seconds (without alignments) 84.800 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                 141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KV51 MOUSE
UB48 MOUSE
UB48 HUWAN
YE86 SCHPO
CATG MOUSE
CATG MOUSE
CATG MOUSE
CATG MOUSE
CATG MOUSE
CATG MOUSE
CATG CATG
YBIT YEAST
DGT1 SHEON
YBIT CAGLA
KV3K HUWAN
KV5G MOUSE
K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEUT_YEAST
YA66_METUA
PUR2_CAMJE
NIFN_ANASP
ACFD_ECOLI
SPH2_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSEPU
BPMS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAEEL
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                US-09-635-974A-8
55
1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SwissProt_42:*
                                                                                                          October
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
No.
```

| 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                          | · o                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                              |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------|
| schizosacch<br>strongyloce<br>palinurus v<br>propionibac<br>schizosacch<br>homo sapien<br>vibrio chol<br>actinoplane<br>escherichia<br>selaginella<br>homo sapien<br>mus musculu | ostomi; in V kappa. JUNCTIONS AT A PROTEIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                              |
| 252 85<br>888 98 888 98 98 98 98 98 98 98 98 98 98                                                                                                                               | eostom<br>nae; N<br>jin v<br>junci<br>1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                              |
| 014301<br>P815552<br>P81653<br>P911653<br>Q94794<br>Q14432<br>Q914434<br>P91867<br>P91867<br>P91898<br>P01598                                                                    | a; Euteleostomi; ae; Murinae; Mus noglobulin v kalanism."; SPLICE JUNCTIO CODE FOR A PROTICE FOR A P |                              |
|                                                                                                                                                                                  | TEGIT CO. L.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                              |
|                                                                                                                                                                                  | e)  muri muri muri cd im con me cossIB woul  Y-DET  Y-DET  Y-DET  TE00  11, L  134; L                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                              |
| S                                                                                                                                                                                | uence update) otation update) oration update) recursor (Fragment). Craniata; Vertebrata Sciurognathi; Muridat and rearranged immu alized mutation mecha alized mutation mecha alized mutation by REG RAPPA CHAIN V-V REG GKAPPA CHAIN V-V REG COMPLEMENTARITY - DETERNAMENCRK-1. COMPLEMENTARITY - DETERNAMENCRK-3.                                                                                                                                                                                                                                           | 1173 AA.                     |
| S. SCHPO M. STRPU M. STRPU B. PROFR 4. SCHPO A. HUMAN D. A. HUMAN B. ACTMI B. ACTMI A. ECLMO F. HUMAN V. MOUSE ALIGNMENTS                                                        | PRT; 115 A  quence update notation upda precursor (Fr Craniata, Ve Sciurognathi 318; ", Zachau H.G e and rearran ca lized mutat AR TO BE TWO THE ALTERNAT THE ALTERNAT FRAMEWORK-1 COMPLEMENTARI FRAMEWORK-2 COMPLEMENTARI FRAMEWORK-3 COMPLEMENTARI FRAMEWORK-3 COMPLEMENTARI SY SIMILARITY CITBECTSSCS SCORE SO; DB Pred; No: 0.0 pred; Nismatches i Mismatches i                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                              |
| YE85 SCHPO WUSM STREPU HCY PALVU MUTB PROFR ORC4 SCHPO CN3A HUMAN ACPD VIBCH XYLB ACTWI XYLB ACTWI CHLB SELWO KVIF HUMAN KV3V MOUSE ALIGNMEN                                     | PRT; 115 AA.  ated) : sequence update) : annotation update) L7 precursor (Fragment).  L7 precursor (Fragment).  11 precursor (Fragment).  264318;  11 H., Zachau H.G.;  11 In and rearranged immunoglobul 1 localized mutation mechanism.";  APPEAR TO BE TWO POSSIBLE SPLICE  CON THE ALTERNATE WOULD CODE FOR  Signal; 3D-Structure.  IG KAPPA CHAIN V-V REGION L7.  FRAMEWORK-1.  COMPLEMENTARITY-DETERMINING-1  FRAMEWORK-2.  COMPLEMENTARITY-DETERMINING-1  FRAMEWORK-3.  COMPLEMENTARITY-DETERMINING-2  FRAMEWORK-3.  COMPLEMENTARITY-DETERMINING-3  FRAMEMORK-3.  COMPLEME | PRT;                         |
| AMUKXÞUOZZZK                                                                                                                                                                     | D;<br>Last seed<br>Last seed<br>Last and<br>Lon L7 F<br>cordata;<br>dentia;<br>dentia;<br>dentia;<br>dentia;<br>lon L7 F<br>cordata;<br>dentia;<br>dentia;<br>lon L7 F<br>L1).<br>7-19.<br>11.<br>12.<br>13.<br>14.<br>14.<br>15.<br>16.<br>17.<br>19.<br>19.<br>19.<br>10.<br>11.<br>11.<br>11.<br>11.<br>12.<br>13.<br>14.<br>15.<br>16.<br>17.<br>18.<br>18.<br>19.<br>19.<br>19.<br>19.<br>19.<br>19.<br>19.<br>19                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                              |
| 595<br>637<br>637<br>727<br>972<br>11141<br>1520<br>61<br>89<br>103<br>108                                                                                                       | 8 '.0 '.00 ON BORES '' HIGHARMACOLOGIS T<br>N D TO MODES '' HI HIJOONEADORNEUS COM I N                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | STANDARD;                    |
|                                                                                                                                                                                  | LT 1  WOUSE  WOUSE  FOLG42;  POL642;  10-0CT-2003 (Rel. 01)  11-OCT-2003 (Rel. 42)  II SASSIGTNIN  WE ARDA Chât N. V-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | STA                          |
|                                                                                                                                                                                  | 10.00 (R. R. R. C.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                              |
|                                                                                                                                                                                  | EXT. BOUGE STA MOUSE STA MOUSE STA MOUSE STA MOUSE STA MOUSE STA MOUSE STA STA MOUSE STA M | MOUSE                        |
| #10.00.00.010.m#10                                                                                                                                                               | SEULT 1  SEULT 1  V51 MOUSE  P01642; P01642; P1 21-JUL-19  10-OCT-20  E 10-OCT-20   | MOUSE<br>UB4B                |
|                                                                                                                                                                                  | RESULT STATE THE THE TENT OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | UB4B_MOUSE<br>ID _UB4B_MOUSE |
|                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                              |
|                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                              |

a

```
tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; ; EMBL; ; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
EMBL;
                                                                           ----
A Ckazaki Y., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Raddo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yamaru Y., Puruno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Raddarelli R., Hill D.P., Bult C., Hame D.A., Canchach J., Golobori T., Baldarelli R., Hill D.P., Bult C., Hattalov S., Beisel K.W., Badta D., Brusic V., Chothia C., Corbani L.E., Cousins S., Balta E., Dragani T.A., Fletcher C.F., Forrest A., Farzer K.S., Armani A., Kawali H., Fletcher C.F., Forrest A., Gough J., Grani, A., Kawaji H., Gissi C., Godzik A., Gough J., Armani A., Kawaji H., Gissi C., Godzik A., Gough J., Armani A., Kawaji H., Markanawa N., Jackson I.J., Jarvis E.D., A. Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Magoltt D.R., Maltais L., Marchionni L., McKenzie L., Mki H., Masashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pecole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Rald J., King B.Z., Ringwald M., Sandelin A., Schneider C., Sengle C.A., Setou M., Shimada K., Wanner L., Wahlestedt C., Wang Y., Watanaband M., Suran Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hincoane, Kishikawa T., Konno H., Nakamura M., Saakaume N., Satowa I., Maraa A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Maraa A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Maranishi K., Sakai D., Shibate K., Shibada K., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21626129; PubMed=11770485;
Mack T.G.A., Reiner M., Beirowski B., Mi W., Emanuelli M., Wagner D.
Thomson D., Gillingwater T., Court F., Conforti L., Fernando F.S.,
Tarlton A., Andressen C., Addicks K., Magni G., Ribchester R.R.,
"Wallerian degeneration of injured axons and synapses is delayed by in Ube4b/Numat chimeric gene.";
Nat. Neurosci. 4:1199-1206(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., Birney E., Hayashizaki Y., Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/Ola; TISSUE=Brain;
MDDLINES-2048194; PubMed=11027338;
Conforti L., Tarlton A., Mack T.G.A., Mi W., Buckmaster E.A.,
Wagner D., Perry V.H., Coleman M.P.;
Wagner D., Perry V.H., Coleman M.P.;
Wagner D., Perry Willineric protein and overexpression of Rbp7 in the slow Wallerian degeneration (Mids) mouse.";
Proc. Natl. Acad. Sci. U.S.A. 97:11377-11382(2000).
                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION, AND ROLE IN DELAY OF WALLERIAN DEGENERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Characterization of the mouse gene for the U-box-type ubiquitin
                     10-ocr-2003 (Rel. 42, Created)
10-ocr-2003 (Rel. 42, Last sequence update)
10-ocr-2003 (Rel. 42, Last annotation update)
Ubiquitin conjugation factor E4 B (Ubiquitin-fusion degradation
protein 2) (Ufd2a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., SUBUNIT, SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko C., Hatakeyama S., Matsumoto M., Yada M., Nakayama K.,
Nakayama K.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iochem. Biophys. Res. Commun. 300:297-304 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUB=Testis;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22392632; PubMed=12504083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 420:563-573(2002)
                                                                                                                                                                          musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ligase UFD2a."
                                                                                                                         protein 2) (U
                                                                                                                                                                               Mus
```

DDTTTO

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., TAS
                                                                                                                                                                                                                                                                                                                                                                                                        PTM: Proteolytically cleaved by caspases during apoptosis. Cleaved efficiently at Asp-123 by caspase-6 and granzyme B. Cleaved with approximately 10-fold less efficiency at Asp-109 by caspase-3 and caspase-7 (By similarity).

MISCELLANBOUS: In strain C57BL/Ola, an 85-kb region on chromosome 4 containing Numat and Ube4b is triplicated. Ube4b becomes linked to Numat and encodes a fusion protein located in the nucleus which is responsible for the delayed Wallerian degeneration of injured
FUNCTION: Binds to the ubiquitin moleties of preformed conjugates and catalyzes ubiquitin chain assembly in conjunction with E1, E2, and E3 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE UBIQUITIN CONJUGATION FACTOR E4 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R GO; GO:000151; C:cytoplasm; IDA.
R GO; GO:000151; C:ubiquitin IDA.
R GO; GO:000151; C:ubiquitin IDA.
R GO; GO:000151; C:ubiquitin IDA.
R GO; GO:0003754; P:chaperone activity; NAS.
R GO; GO:001989; F:enzyme binding; IPI.
R GO; GO:0006840; P:ubiquitin conjugating enzyme activity; TAS.
R GO; GO:0006815; P:protein conjugating enzyme activity; TAS.
R GO; GO:0006417; P:protein folding; NAS.
R GO; GO:0042787; P:protein folding; NAS.
R GO; GO:0042787; P:protein folding; NAS.
R GO; GO:0042787; P:protein toliquitination during ubiquitin-dep. .; T
R GO; GO:0042787; P:protein folding; NAS.
R GO; GO:0042787; P:protein folding; NAS.
R GO; GO:0042787; P:protein folding; NAS.
R InterPro; IPROJA614; U-box; I.
R PFam; PRO4564; U-box; I.
                                                                                                                                                                                     and by the state with Vcp.
SUBCELLULAR LOCATION: Cytoplasmic.
IISSUE SPECIFICITY: Expressed predominantly in neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP260924; AAG17285.1; ALT_TERM.
EMBL; AP260926; AAG17287.1; ...
EMBL; AP260927; AAG38492.1; ...
EMBL; AB083244; BAC56586.1; ...
EMBL; AB083249; BAC56586.1; JOINED.
EMBL; AB083249; BAC56586.1; JOINED.
EMBL; AB083250; BAC56586.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, ABOU32255 BAC56586.1; JOINED. BMBL, ABO032255 BAC56586.1; JOINED. BMBL, ABO032251 BAC56586.1; JOINED. BMBL, ABO03229; BAC56586.1; JOINED. BMBL, ABO03229; BAC56586.1; JOINED. BMBL, ABO03261; BAC56586.1; JOINED. BMBL, ABO03270; BAC56586.1; JOINED. BMBL, ABO03271; BAC567211; JOINED. BMBL, AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB083252; BAC56586.1;
AB083253; BAC56586.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAC56586.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro, IPR003613; Znf-
Pfam; PF04564; U-box; 1.
SMART; SM00504; Ubox; 1.
Ubl conjugation pathway.
DOMAIN 1102 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in C57BL/0]
```

```
ö
  (BY
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lubyova B., Onyango P., Kurzbauer R., Lummerstorfer J.A., Kleiner B., Gardellin P., Willhoeft U., Weith A.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                            (BY CASPASE-6 AND GRANZYME B)
  (BY CASPASE-3 AND CASPASE-7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The human homologue of the yeast polyubiquitination factor Ufd2p cleaved by caspase 6 and granzyme B during apoptosis."; Biochem. J. 361:587-595(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UB64B HUMAN STANDARD; PRT; 1302 AA.
055155; 075169; 095338; 0960D4; Q9BYI7;
28-FEB-2003 (Rel. 41, Create sequence update)
26-FEB-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Ubiquitin conjugation factor E4 B (Ubiquitin-fusion degradation protein 2) (Homozygously deleted in neuroblastoma-1).
UBE4B OR UFD2 OR HDNB1 OR KIAA0684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, MUTAGENESIS ASP-109; ASP-121 AND ASP-123, AND CLEAVAGE BY CASPASES.
MEDLINES=11661475; PubMed=11802788;
MANDORRY J.A., Odin J.A., White S.M., Shaffer D., Koff A., Casciola-Rosen L., Rosen A.;
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98403880; PubMed=9734811;
Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                           ; DB 1; Length 1173; . 18;
                                                                                                     L -> P (IN REF. 1).
D -> B (IN REF. 3; BAC26672).
S -> T (IN REF. 3; BAC26672).
C -> Y (IN REF. 3; BAC26672).
E -> K (IN REF. 3; BAC26672).
Z MW; 153853C06372F6CD CRC64;
                                                                                                                                                                                                                          3; BAC26672).
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martin S.; submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1112-1302 FROM N.A.
Barrow I.K.-P., Boguski M.S., Touchman J., Spencer F.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                       SIMILARITY).
CLEAVAGE (BY CAS
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                           Score 37; DB 1
Pred. No. 18;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 102-1302 FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Substantia nigra;
Kageyama H., Ohira M., Nakagawara A.;
"Human ubiquitination factor E4/UFD2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                code for large proteins in vitro."; DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                              67.38;
                                                                                                                                                                                                                                                                                                                                      66.78;
                                                                                                                                                                                                                                                        133302
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                            697
                                                        124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
                                                                                                                                                                                                                                                                                                                                                                                                                            3 SOSIGINIH 11
                                                                                                           298 29
408 40
674 67
697 69
753 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOSLGLNVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                     123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain,
                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
UB4B HUMAN
                                                     SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The
899999999
                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCOORDING TO THE SECTION OF THE SEC
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLEAVAGE (BY CASPASE-3 AND CASPASE-7).
CLEAVAGE (BY CASPASE-6 AND GRANZYME B).
Missing (in isoform 3).
Missing (in isoform 2).
Missing (in isoform 2).
FIIG-VSP 007102.

FIIG-VSP 007102.

- GKWIH (in isoform 3).

FIIG-VSP 007103.

- AGWITION OF CLEAVAGE BY CASPASE-3
                                                                                                                                                                                                               Isode-095155-3; Sequence=VSP_007101, VSP_007102, VSP_007103;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Highest expression in ovary, testis, heart and skeletal muscle. Expression is low in colon, thymus and peripheral blood leukocytes. Almost undetectable in lung and spleen.
PTM: Proteolytically cleaved by caspases during apoptosis. Cleaved efficiently at Asp-123 by caspases during apoptosis. Cleaved approximately 10-fold less efficiency at Asp-109 by caspase-3 and
FUNCTION: Binds to the ubiquitin moleties of preformed conjugates and catalyzes ubiquitin chain assembly in conjunction with E1, E2, and E3 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D->A: ABOLITION OF CLEAVAGE BY CASPASE-6.
NO EFFECT ON CLEAVAGE BY GRANZYME B.
D->A: ABOLITION OF CLEAVAGE BY CASPASE-6
                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE UBIQUITIN CONJUGATION FACTOR E4 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005737; C:cytoplasm; ISS.
GO; GO:000151; C:ubiquitin ligase complex; TAS.
GO; GO:000151; C:ubiquitin ligase complex; TAS.
GO; GO:00013754; F:chaperone activity; ISS.
GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
GO; GO:0006815; P:apoptosis; IDA.
GO; GO:0006815; P:apoptosis; IDA.
GO; GO:0006457; P:protein folding; ISS.
GO; GO:0004578; P:protein folding; ISS.
GO; GO:00042787; P:protein ubiquitination during ubiquitin-dep.
GO; GO:0009411; P:response to UV; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 1; Length 1302;
Pred. No. 20;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6BAA80984B03E43B CRC64;
                                                    -1- SUBUNIT: Interacts with Vcp (By similarity).
-1- SUBCELULIAR LOCATION: Cytoplasmic (By similarity).
-1- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ubl conjugation pathway, Alternative splicing.
DOMAIN 1231 1293 UBOX.
                                                                                                                                                                                  IsoId=095155-2; Sequence=VSP_007102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND CASPASE-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND GRANZYME
                                                                                                                                               IsoId=095155-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF331520; AAK69622.1; -.
EMBL; AF043117; AAADC233.1; -.
EMBL; ABC28839; BA840446.1; -.
EMBL; AL096841; CAC42394.1; -.
EMBL; AB014584; BAA31659.2; -.
EMBL; AF091093; AAC72962.1; ALT_SEQ.
Genew; HGNC:12500; UBE49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1302 AA; 146183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00504; Ubox; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF04564; U-box; 1
SMART; SM00504; Ubox; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1234
                                                                                                                             Name=1;
                                                                                                                                                                                                     Name=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGEN
                                                                                                                                                                                                                                                                                                                -
```

```
SO
                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARAINING TO STANDING TO STAND THE STANDING TO STANDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaces,
Schizosaccharomyces.
                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical protein C9G1.06c in chromosome I.
                                                                                                                                                                                              886 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, Z98763; CAB11490.1; -.
PIR, T39229; T39229.
HSSP, P29355; 1SEM.
GGeneDB SPombe; SRC9G1.06c; -.
INTERFO; IPR001452; SH3.
InterPro; IPR002931; Trnsglumase_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE, PSS0002; SH3; 1.

Hypothetical protein; SH3 domain.

6 67 SH3.
                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seqn
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3; 1.
                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00326; SH3; 1.
SMART; SM00460; TGC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00018; SH3; 1.
                                                    50 SOSLGLNVH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                        SPAC9G1.06C
                                                                                                                                                                                            SCHPO
                                                                                                                                                                                            YE86 SCH
014302;
                                                                                                                                                                                         PALD BARRAR BARA
                                                 g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the EMBL outstants. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Swiss Webster; TISSUE=Connective tissue;
MEDINIP=93200524; PubMed=8453108;
MEDINIP=93200524; PubMed=8453108;
Heusel J.W., Scarpati E.M., Jenkins N.A., Gilbert D.J., Copeland N.G.,
Shapiro S.D., Ley T.J.;
Molecular cloning, chromosomal location, and tissue-specific
expression of the murine cathepsin G gene.";
Blood 81:1614-1623 (1993).
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINELS 2. 1-0.

Makamura N., Tsuru A., Hirayoshi K., Nagata K.;

Makamura N., Tsuru A., Hirayoshi K., Nagata K.;

Murification and characterization of a vimentin-specific protease in mouse myeloid leukemia cells. Regulation during differentiation and identity with cathepsin G.";

Bur. J. Blochem. 205:1947-994 (1992).

Fur. J. Blochem. 205:1947-994 (1992).

-I- FUNCTION: This vimentin filaments; occurring during cell differentiation of vimentin filaments; occurring during cell differentiation, movement and mitosis.

-I- CATALYTIC ACTIVITY: Specificity similar to chymotrypsin C.

-I- SUBCELLULAR LOCATION: STRONGIY ASSOCIATED WITH MEMBRANES.

-I- SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last amocation update)
Cathepsin G precursor (EC 3.4.21.20) (Vimentin-specific protease)
                                                                                                                                                                             .
0
                                                                                                 Query Match 65.5%; Score 36; DB 1; Length 886; Best Local Similarity 85.7%; Pred. No. 21; Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kulmburg P., Baumruker T., Werner F.;
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Leaden X A1,
Huang R., Aveskogh M., Hellman L.T.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
610 POLY-SER.
98262 MW; D0C4879C1882E869 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M96801; AAA37376.1; -.
EMBL; X70057; CAA49661.1; -.
EMBL; X78544; CAA55290.1; -.
PIR; S40162; 840162.
HSSP; P09311; 1CGH.
MEROPS; S01.133; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                    451 SVGTNIH 457
                                 886 AA;
                                                                                                                                                                                                                                                    5 SIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE OF 21-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATG MOUSE
P28293;
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
CATG_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (VSP)
```

```
DNA recombination; Coiled coil; Complete proteome.

DOMAIN 29 88 COILED COIL (POTENTIAL).

SEQUENCE 432 AA; 48721 WW, 73DF45A996A2F692 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z00021; CAA77316.1; -. PIR; A01899; K3HU41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.0%;
                                                                                                                         Local Similarity 66.7 les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 60.0 les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RASOSIGTNI 10
                                                                                                                                                                                                                                                357 SOKIGNNLH 365
                                                                                                                                                                                                3 SQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 RASOSVSSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KV3K_HUMAN
ID KV3K_HUMAN
AC P06311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
NON TER
SEQUENCE
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2009-2008(2001).
-!- FUNCTION: Involved in DNA recombination (By similarity).
-!- SIMILARITY: Belongs to the rmuc family.
                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
MEDLINE=21442074; Renesto-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
MGD; FL.

INTERPRO; IPR00125...
INTERPRO; IPR00134; Pept...

REALY, PRO0025; CHYMOTRYPSIN.

AR RAINT; PR00025; CHYMOTRYPSIN.

AR RANGT; PS00134; TRYPSIN BOW; 1.

BROSITE; PS00134; TRYPSIN BIS.; 1.

BROSITE; PS00134; TRYPSIN BIS.; 1.

WHYDROIAS; Serine protease; Zymogen; Glycoprotein; Signal; WHYDROIAS; PROSITE; PS00134; TRYPSIN BIS.; 1.

FY HYDROIAS; PROPER BIS.; 1.

FY SIGNAL 1 18 WENDERNEY; 1.

FY CHAIN 21 261 CCHARGE RELAY SYSTEM (BY SIMILA ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILA ACT_SITE 201 201 CHARGE RELAY SYSTEM (BY SIMILA ACT_SIMILA ACT_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 1; Length 261; Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> S (IN REF. 4)
-> G (IN REF. 4)
-> P (IN REF. 4)
-> P (IN REF. 4)
5EFAIAGEIOSIDDFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ar recombination protein rmuC homolog.
RMUC OR RC1057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE008657; AAL03595.1; -. PIR; A97832; A97832. InterPro; IPR003798; DUF195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29095 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.6
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ||| |||:
149 RVSQSRGTNV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RASQSIGTNI 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02646; RmuC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMUC RICCN
Q92GR5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
RMUC RICCN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license@aspeement (See http://www.isb-sib.ch/announce/or send an email to license@aspeement (See http://www.isb-sib.ch/announce/or send an email to license@aspeement (See http://www.isb-sib.ch/announce/
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·.
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG KAPPA CHAIN V-III REGION IARC/BL41. PRAMENORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMENORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

BEDLINESERS614852, PubMed=2997711,

Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;

"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING-2
63.6%; Score 35; DB 1; Length 432; 66.7%; Pred. No. 16; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 128;
Pred. No. 7.7;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14070 MW; CC8957F0FE3B9012 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 seppa chain V-III region IARC/BL41 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSP, PO1607; INEI.
GO, GO: 0005576; C:extracellular; NAS.
GO, GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR03596; Ig_v.
Pfam; PP00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 13:6499-6513(1985).
```

φ

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RX MEDLINE=20196006, PubMed=10731132,
RATH=BBEREALELY,
RAD Adams M.D., Celniker S.B., Holt R.A., Bvans C.A., Gocayne J.D.,
RAD Adams M.D., Celniker S.B., Holt R.A., Bvans C.A., Gocayne J.D.,
RAD Adams M.D., Celniker S.B., Holt R.A., Banburner M., Henderson S.N.,
Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chan L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
RAD Ballew R.M., Basul A., Baxendale J., Bayaktaroglu L., Beaaley E.M.,
Ballew R.M., Banns P.V., Berns B.D., Bhandari D., Blandari D.,
RAD Ballew R.M., Banns D.V., Berns B.D., Bhandari D., Bottier P.,
RAD BORON K., Dough L.E., Downes M. Durgh R.D., Dew I., Dietz S.M.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RAD Boron K., Dough LE., Downes M. Dugan-Rocha S., Dunkov B.C., Dunn P.,
RAD Boron K., Dough LE., Downes M. Dugan-Rocha S., Dunkov B.C., Dunn P.,
RAD Boron K., Dough LE., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RAD Boron K.J., Bayangelista C.C., Ferriaz C., Ferriar S., Dunko M. S.,
RAD Boron K.J., Bayangelista C., Stannison J., Rolled M., A.,
RAD Boron K.J., Bayangelista C., Stannison J., Marsel M., Lidali M., Kalush F., Karpen G.H., Kaz C., Kannison J., Brownes M. J.
RAD Boron K.J., Harvey D.A., Howland T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Weim M.P., McDerson D.L.,
RAD Minnel B.B., McIntoen T.C., McLeod M.P., McPherson D.L.,
RAD Merkulov G., Milshina N.V., Mobarry C., Morris J., Mospan P.,
Reinert K., Remington K.A., Mixon K., Nusskern D.R., Parle D.Y.,
Rad R., Tector C., Turner R., Venter B., Wang X.,
Williams S.M., Woodage T., Stanner R., Wang A.H., Wang X.,
Walliams S.M., Woodage T., Shan M., Zhong W., Zhon G., Zhu K., Shander S.M., Reiner K., Zhong W., Zhon G., Zhu K., Shander S.M., Woodage T., Worley K.C., W.,
Radibbs R.A., Wyers E.W., Wholl M., Wooday C.J., Wellen G., Scheeler T., Shan M., Zhong K., Wallen S., Shander S.M., Woodage T.W., Worley K.C., W.,
Radibbs R.A., Wyers E.W., Wallen G., Scheeler S., Scheeler S.,
Radibs R.A., Wyers E.W., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS.
MEDLINE=22426069; PubMed=12537572;
Mistar S., Crosby M., Mungall C.J., Matthews B.B., Campbell K.S.,
Mistar S., Crosby W., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mutations", mear the Trf cluster cause a premeiotic defect in the Drosophila male germ line."; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                             10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence
                                                          252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:2185-2195(2000).
                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crowley T.E.;
                                                          DROME
RESULT 8
TRFP_DROME
ID TRFP_D
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                     STRAIN=Berkeley; TISSUE=Embryo;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R.A., Gonzalez M., Guarin H., Kronmiller B., Li P.W., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J.M., Paragas V., Park S.,
Patel S., Photanenavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.E.;
Submitted (FEB-2003) to the EMBL/GenBank/DDbJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence of a segment of yeast chromosome II shows two novel genes,
                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: May regulate transcription of class II genes through association with the RNA polymerase II-SRB complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-00T-1994 (Rel. 30, Created)
01-00T-1994 (Rel. 30, Last sequence update)
01-N0V-1995 (Rel. 32, Last annotation update)
Hypothetical 40.8 kDa protein in RHKI-PETI12 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                           "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Component of an RNA polymerase II-SRB complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288C;
MEDLINE=96076635; PubMed=7502586;
Obermaier B., Gassenhuber J., Piravandi B., Domdey H.;
Sequence analysis of a 78.6 kb segment of the left end of
Saccharomyces cerevisiae chromosome II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 252;
Pred. No. 15;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, Y10975, CAA71871.1; -.
EMBL, AE003619; AAF2599.2; -.
EMBL, BT003473; AA039476.1; -.
FlyBase; FBGM0013531; Trfp.
Transcription regulation; Nuclear protein.
CONFLICT 220 H -> Q (IN REF. 1).
SEQUENCE 252 AA; 27862 WW; 608AB5A43DAC52F5 CRC64;
                                                                                    Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                similarity). -
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95274327; PubMed=7754714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keast 11:1103-1112(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 SQQVGPNVH 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                        systematic review.
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                         similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cusick M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YBI1 YEAST
P38180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
```

ö

```
InterPro; IPR003607; Met_phsphohydro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter J.C.;
                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thaliana.
                                                                                                                                                                                                                                                                                                                                                            P45951
                                                                                                                                                       Best Loca
Matches
   DA DA DA S
                                                                                                                                                                                                           ò
                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MR-1;
MEDLINE22297686; PubMed=12368813;
Meidelberg JF., Paulsen ITT. Nelson K.E., Gaidos E.J., Nelson W.C.,
Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
DeBoy R.T., Dodson R.J., Dumayam L.A., White D.H., Kolonay J.F.,
Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.,
"Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shewanella oneidensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Deoxyguanosinetriphosphate triphosphohydrolase-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence";
Shewanella oneidensis.";
Nat. Biotechnol. 20:1118-1123(2002).
-!- SIMILARITY: Belongs to the dGTPase family. Subfamily 2.
                                                                                                                                                                                                                                                                                                                                                                                              61.8%; Score 34; DB 1; Length 368; 77.8%; Pred. No. 23; 1. Mismatches 1; Indels
one almost entirely hydrophobic and the other extremely asparagine-serine rich.", Yeast 10:1251-1256(1994).
                                                                                                                                                                                                                                                                                                                                                            40767 MW; D52EAA7AD85C5D14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF 01212; -; 1.
InterPro; IPR006261; dGTP_triPase.
InterPro; IPR006674; HD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE015690; AAN55516.1; -.
TIGR; SO2485; -.
                                                                                                                                                                                                                       EMBL, X79489; CAA56026.1; -. EMBL, Z35842; CAA84902.1; -. EMBL, M89908; AAA75353.1; -. PIR; S46601; S46601.
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                            Germonline; 138516; -- SGD; S0000177; YBL081W. Hypothetical protein. SEQUENCE 368 AA; 4076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 SSSIGTNIN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHEON
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGT1 SHE
Q8EEA2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
DGT1_SHEON
ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics, and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 10-536 FROM N.A.

SEQUENCE OF 10-536 FROM N.A.

STATISTORY COlumbia, TISSUB-Callus;

MEDLINE-94211851; PubMed=7512780;

MEDLINE-94211851; PubMed=7512780;

Rabiychuk E., Kushnir S., van Montagu M., Inze D.;

The Arabidopsis thaliana apurinic endonuclease Arp reduces human transcription factors Fos and Jun.";

Transcription factors Fos and Jun.";

Proc. Natl. Acad. Sci. U.S.A. 91:3299-3303(1994).

Tedox factor: Is multifunctional and may be involved both in DNA repair and in the regulation of transcription.

Tedox factor: Is multifunctional and may be involved both in DNA repair and in the regulation of transcription.

Tedox factor: The C-O-P bond 3' to the apurinic or apprinted in DNA is broken by a beta-elimination reaction, leaving a 3'-terminal unsaturated sugar and a product with a perminal 5'-phosphate.

Terminal 5'-phosphate.

TESUE SPECIFICITY: Expressed in the siliques, flowers, and stems.

High level expression is seen in the leaves.

High level expression is seen in the leaves.

SEMILARITY: Contains 1 SAP domain.
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Columbia;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J. B., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                     61.8%; Score 34; DB 1; Length 441; 54.5%; Pred. No. 27; 3; Indels ive 2; Mismatches 3; Indels
Pfam; PF01966; HD; 1.
SWART; SW00471; HDc; 1.
TIGRFAMS; TIGR01353; dGTP LriPase; 1.
Hypothetical protein; Hydrolase; Complete proteome.
SEQUENCE 441 AA; 50619 WW; CIDA17F434ED9514 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                           399 RASEQLGLNSH 409
                                                                                                                                                                                                                                                                                                                                                                         1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
PRESULT 11
PARATH
TAP PARATH
TAP PARATH
TO 1-NO
DT 10-NO
DT 30-MAD
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-88274327; PubMed=2839594;
MEDLINE-88274327; PubMed M.A., Davison A.J., Dolan A., Frame M.C.,
MCGOCh D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
MCNab D., Perry L.J., Scott J.B., Taylor P.;
"The complete DNA sequence of the long unique region in the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-!- FUNCTION: Tegument protein.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                              EMBL; AC04221; AAF36067.2; -
BEMBL; AC04221; AAF36067.2; -
WormPep; Y76B12C.7; CE29932.

GO; GO:0005847; C:mENA cleavage and polyadenylation specificity factor.
GO; GO:0005364; F:cleavage/polyadenylation; NAS.
GO; GO:0006378; P:mRNA polyadenylation; NAS.
Interpro; IPR00471; CPSF_A_C.
Pfam; PF03178; CPSF_A, 1.
mRNA processing; Nuclear protein; RNA-binding.
SEQUENCE 1454 AA; 162716 MW; DEFEF8BB2FFBD16F CRC64;
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q. 3164 AA; 335857 MW; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                                           Score 34; DB 1; Length 1454;
Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-ARR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein UL36).
                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 3164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, X14112; CAA32311.1; -.
PIR, I30085; WMBEH6.
InterPro; IPR066528; Herpes_teg_N.
InterPro; IPR065210; Herpes_Ui36.
Pfam; PF04443; Herpes_teg_N, I.
Pfam; PF03586; Herpes_Ui36; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.8%;
                                                                                                                                                                                                                                              63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66...
Gronservative
                                                                                                                                                                                                                                                                                                               1307 RAAINIGTNIN 1317
                                                                                                                                                                                                                                              Best Local Similarity 63.6
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                            1 RASOSIGINIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10299;
                                                                                                                                                                                                                                                                                                                                                                                                 TEGU HSV11
P10220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat.
                                                                                                                                                                                                                                                                                                                       d
         ò
                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                            DNA repair; Lyase; Nuclear protein.
DOMAIN 1 278 HIGHLY CHARGED; INCREASES THE AFFINITY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                  MAGNESIUM OR MANGANESE (BY SIMILARITY)
GENERAL BASE (BY SIMILARITY).
SCIFC17EA991D27B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Last sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
Probable cleavage and polyadenylation specificity factor, 160 kDa subunit (CPSF 166 kDa subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 1; Length 536;
Pred. No. 33;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRANT=Bristol N2;
Cordes M.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                    AP ENDONUCLEASE.
                                                                                                                                                       Pfam, PF03372; Exc_endo_phos; 1.
Pfam, PF02037; SAP; 1.
SMART, SM0513; SAP; 1.
SMART, SM0513; SAP; 1.
TIGRFAMS; TIGR00195; excDNase_III; 1.
TIGRFAMS; TIGR00633; xth; 1.
PROSITE; PS00726; AP_NUCLEASE_F1 1; 1.
PROSITE; PS00727; AP_NUCLEASE_F1 2; 1.
PROSITE; PS00800; SAP; 1.
                                                                                                                                                                                                                                                                                                                           ARP FOR DNA
         or send an email to license@isb-sib.ch)
                                 EMBL; AC004625; AAC23731.1; -.
EMBL; X76912; CAA54234.1; -.
PIR; 702441; T02441.
HSSP; P27695; 1E9N.
InterPro; IPR000097; APendonclsel.
InterPro; IPR001089; Exo endo phos.
InterPro; IPR001088; ExoIII_xth.
InterPro; IPR003034; SAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                    60260 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                      313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          506 SOSIAANVH 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                       97
279
313
327
527
536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS
                                                                                                                                                                                                                                                                                                                                                                      METAL
ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y76B12C.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPSA CAE
Q9N4C2;
                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                         DOMAIN
         g
```

ĕ

ô

1401 RAEQALGIN 1409

셤

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Lucopean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                               STRAIN=IL1403;
MEDLINE=1225186; PubMed=11337471;
MEDLINE=2.25186 P. Mauger S., Jaillon O., Malarme K.,
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
                                                                                                                  Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P., Goldfien R., Carson D.A., "Cloning and sequence determination of a human rheumatoid factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-1987 (Rel. 04, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-lli region CLL precursor (Rheumatoid factor).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 1; Length 87; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; B86743; B86743.

HAWAP; ME_01054; -; 1.

InterPro; IPR002912; ACT.

Pfam; PF01842; ACT; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 87 AA; 9282 MW; A77ED01657C149DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                light-chain gene.";
Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
                                                                                                                                                                                                                                                                                                       lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
-!- SIMILARITY: Belongs to the UPF0237 family.
                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypotherical UPF0237 protein yjhc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86177570; PubMed=3083417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE006329; AAK05044.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.08;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RASOSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :::| |||
64 RKGEALGVNIH 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                          LUHC OR LL0946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KV3H HUMAN
P04207;
 LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KV3H HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                   à
```

```
ö
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                            IG KAPPA CHAIN V-III REGION CLL. FRANEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRANEWORK-2. COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      5C13B411BE60CC14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 1;
Pred. No. 13;
2; Mismatches 2
                                                                                                                       GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                           Pfam, PF00047; ig; 1. --
SMART; SM00406, IGV; 1.
PROSITE, PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                         129
14275 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%;
                                                                                               EMBL; M12740; AAA58992.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Query Match
Best Local Similarity 60.00,
                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                     SIGNAL
```

6, 2004, 16:30:27 Search completed: October Job time: 8.75439 secs

ö

1 RASOSIGTNI 10

ò d

44 RASOSVSNNL

This Page Blank (uspio)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

6, 2004, 16:23:59; Search time 11.5789 Seconds (without alignments) 91.382 Million cell updates/sec October Run on:

US-09-635-974A-8 55 1 RASQSIGTNIH 11 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 1   |       | æ (     |        |    | SOUTHERES |                    |
|-----|-------|---------|--------|----|-----------|--------------------|
| No. | Score | Query   | Length | 90 | · QI      |                    |
| -   | 50    | 900     | 60     | 7  | PH1082    | Iq light chain V r |
| N   | 20    | 90.9    |        | Н  | KVMSL7    | Ig kappa chain pre |
| m   | 50    | 。       | 12     | 7  | PN0445    | Ig kappa chain pre |
| 4   | 48    | 7.      | 10     | 7  | C30502    | Ig kappa chain v r |
| Ŋ.  | 44    | ö       | 11     | 7  | 966008    | Ig kappa chain pre |
| 9   | 42    | 76.4    | 10     | 7  | S26346    | Ig kappa chain v r |
| ۲   | 42    | Ġ.      | 10     | ~  | B43413    | Ig kappa chain V r |
| œ   | 42    | Ġ       | 10     | ~  | B45722    | anti-glycoprotein  |
| 0   | 42    | ý.      | 10     | ~  | A45722    | anti-glycoprotein  |
| 2   | 42    | ů.      | 13     | 7  | A26471    | Ig kappa chain pre |
| 디   | 41    | 4.      | 10     | 7  | C45722    | anti-glycoprotein  |
| 12  | 40    | ά.      | σv     | ~  | PH0867    | Ig kappa chain V r |
| 13  | 39    |         | o      | 7  | 837511    | Ig kappa chain V r |
| 14  | 39    | ö       | 21     | ~  | JE0243    | Ig kappa chain NIG |
| 5   | 38    | φ.      | 12     | ~1 | S40370    | Ig kappa chain - h |
| 9   | 38    | ٩.      | 12     | ~  | S40317    | Ig kappa chain - h |
| 7   | 38    | 9       | 14     | ~  | B30502    | Ig heavy chain V r |
| 80  | 37    | 7.      | 11     | 7  | A25924    | Ig kappa chain pre |
| 6   | 37    | ۲,      | 12     | 0  | 804577    | cappa              |
| 20  | 36    | ъ.      | 44     | ~  | AD3173    | hypot              |
| 7   | 36    | 'n.     | 88     | ~  | T39229    | hypothetical prote |
| CJ. | 35    | ۳,      | æ      | 7  | S16827    | Ig kappa chain V r |
| 33  | 35    | ω,      | æ      | 7  | A37262    | hain V             |
| 24  | 35    | ω.      | 11     | ~  | B26555    | Iq kappa chain V-I |
| ເກ  | 35    | ۳,      | 16     | ~  | S43762    | nding              |
| 9   | 35    | ω,      | 25     | 0  | T52352    | al pře             |
| 7   | 35    | ë.      | 56     | ~  | S40162    | cathepsin G (EC 3. |
| œ   | 35    | ص       | 43     | N  | A97832    | etical prote       |
| 6   | 35    | ٠.<br>س | 98     | 0  | T06576    | rot                |
|     |       |         |        |    |           |                    |

| kappa chain V | kappa chain V | kappa chain V | kappa chain V | kappa chain V |        | kappa chain V | kappa chain | in V   | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S78489        | 834099        | S16834        | S16836        | S16839        | S16828 | S16835        | C28195        | S16824        | S16829        | S34098        | 837525        | 837527        | PH0868        | PL0267      | A28195 |
| 7             | 7             | 7             | ~             | ~             | 7      | ~             | 7             | 7             | 7             | 7             | ~             | 7             | 0             | (7          | N      |
| 83            | 84            | 86            | 86            | 86            | 86     | 98            | 98            | 86            | 86            | 87            | 91            | 91            | 95            | 106         | 107    |
| œ             | 51.8          | 61.8          | 61.8          | 61.8          | 61.8   | 61.8          | 61.8          | 61.8          | 61.8          | 61.8          | 61.8          | 61.8          | 61.8          | 61.8        | 61.8   |
| 61            | •             |               |               |               |        |               |               |               |               |               |               |               |               |             |        |
|               |               | 34            | 34            | 34            | 34     | 34            | 34            | 34            | 34            | 34            | 34            | 34            | 34            | 34          | 34     |

## ALIGNMENTS

RESULT 1

| - |                                                                                     |     |
|---|-------------------------------------------------------------------------------------|-----|
|   | PH1082                                                                              |     |
| _ | Ig light chain V region (clone 165.54) - mouse (fragment)                           |     |
|   | C;Species: Mus musculus (house mouse)                                               |     |
|   | C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 21-Jan-2000         |     |
|   | C;Accession: PH1082                                                                 |     |
|   | R; Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.                               |     |
|   | J. Exp. Med. 176, 761-779, 1992                                                     |     |
|   | A; Title: Both IqM and IqG anti-DNA antibodies are the products of clonally selecti | cti |
|   | A; Reference number: PH0971; MUID: 92381444; PMID:1512540                           |     |
|   | A; Accession: PH1082                                                                |     |
|   | A;Status: nucleic acid sequence not shown                                           |     |
|   | A; Molecule type: mRNA                                                              |     |
| - | A:Residues: 1-87 <til></til>                                                        |     |
|   | A; Experimental source: B cell, strain [NZB x NZW]F1                                |     |
| - | C; Superfamily: immunoglobulin V region; immunoglobulin homology                    |     |
|   | C; Keywords: immunoglobulin                                                         |     |
|   | F;6-80/Domain: immunoglobulin homology <1MM>                                        |     |
|   | Query Match 90.9%; Score 50; DB 2; Length 87;                                       |     |
|   | 45;                                                                                 |     |
|   | Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;                         |     |
|   | Qy 1 RASOSIGTNIH 11                                                                 |     |
|   |                                                                                     |     |
|   | Db 14 RASQSIGTSIH 24                                                                |     |
| • |                                                                                     |     |

ive B (

Is kape chain precursor V region (L7) - mouse (Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A01925
R;Pech, M.: Hochtl, J.; Schnell, H.; Zachau, H.G.
R;Pech and M.; Muller and J.; Muller and rearranged immunoglobulin V-kappa coding seq.
A;Residues: 1018 < PRECA
A;Residues: 1-115 < PRECA
A;Residues: 1-115 < PRECA
A;Residues: 1.15 < PRECA
A;Residues: 1.1

```
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: 526346
R;Stark, S.E; Caton, A.J.
B. Exp. Mad: 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein ep. A;Reference number: S26309; MUID:91341421; PMID:1908510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Accession: B43413

R; Tomiyama, Y; Brojer, B.; Ruggeri, Z.M.; Shattil, S.U.; Smiltneck, J.; Gorski, J.; Kume J. Biol. Chem. 267, 18085-18092, 1992

J; Biol. Chem. 267, 18085-18092, 1992

A; Title: A molecular model of RGD ligands. Antibody D gene segments that direct specificity A; Reference number: A43413; WUID:92388177; PMID:1517241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C,Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 1-114 <STR>
A,Cross-references: EMBL:M27750; NID:g185914; PIDN:AAA58912.1; PID:g553479
A,Note: this sequence was determined from the germline gene
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:91334075
                                     Ristraubinger, B.; Thiebe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G. Biol. Chem. Hoppe-Seyler 369, 601-607, 1988
A; Title: Two unusual human immunoglobulin V-kappa genes.
A; Reference number: 800996; MUID:89134397; PMID:2852016
A; Accession: 800996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Superfamily: immunoglobulin V region, immunoglobulin homology C,Keywords: heterotetramer; immunoglobulin C;F:19/Domain: signal sequence #status predicted <SIG>F:20-114/Product: Ig kappa chain V region #status predicted <P:42-107/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X59211; NID:g52338; FIDN:CAA41921.1; Pl
C;Superfanily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;I4-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Status: preliminary; not compared with conceptual translation A, Molecule type: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: sequence extracted from NCBI backbone (NCBIP:112818)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 76.4%; Score 42; DB 2; Length 102; Local Similarity 72.7%; Pred. No. 0.24; es 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 2;
Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 RASOSIGSSLH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RASOSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RASOSIGINIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 RASÓSISNNLH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-102 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-104 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S26346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 16/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S:
Matches 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: PN0445
R;Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
R;Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymera
A;Reference number: PN0444; MUID:93138402; PMID:1339379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(2050)

(205
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain precursor V-I region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-128 <KAL>
A;Cross-references: GB:L02347
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-10/Domain: signal sequence #status predicted <SIG>
F;1-10/Domain: ignal sequence #status predicted <MAT>
F;26-100/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A)Residues: 1-108 <EIL>
A)Residues: 1-108 <EIL>
A)Cross-references: GB:M21907; NID:g197071; FIDN:AAA38907.1; FID:g197072
C)Supperfamily: immunoglobulin V region; immunoglobulin homology
C)Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IPM>
                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                        Score 50; DB 1; Length 115;
Pred. No. 0.0061;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.3%; Score 48; DB 2; Length 108;
81.8%; Pred. No. 0.015;
iive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 2; Length 128
Pred. No. 0.0069;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain precursor V region (A10) - human (fragment)
C;Species: Homo sapiens (man)
        F;36-110/Domain: immunoglobulin homology <IMM>F;43-108/Disulfide bonds: #status predicted
                                                                                                                        90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.9%;
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                      1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                             44 RASOSIGTSIH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 RASOSIGISIH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||||||||||| 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                  Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: C30502
A, Status: preliminary
A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24
                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

Gaps

.. 0

Gaps

```
C,Accession: PH0867
R,Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
R,Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
A; Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A; Reference number: PH0862; MUID:92078875; PMID:1660528
A; Accession: PH0867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Mesidues: 1-95 - MANA
A;Residues: 1-95 - MANA
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Kaywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;1-23/Region: framework 1
F;1-20/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Date: 22.Sep.1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C,Accession: C45722
R,Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasq. J. Virol. 67, 489-496, 1993
J. Virol. 67, 489-496, 1993
A,Title: Neutrallizing monoclonal antibodies that distinguish three antigenic sites on h. A,Reference number: A45722; WUID:93100833; PMID:7677958
                              Appliance of the sequence of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - mouse (f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115)
C,Species: Mus musculus (house mouse)
C,Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
    R;Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain V region (anti-DNA, R3.5H5G) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1892 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-107 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: sequence extracted from NCBI backbone (NCBIP:120591) (S:Superfanily: immunoglobulin V region; immunoglobulin homology C;Keywords: glycoprotein (S:Keywords: glycoprotein F;Ie-90/Pomain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 2;
Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.5%; Score 41; DB 2;
63.6%; Pred. No. 0.41;
cive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;24-34/Region: complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 72...
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 RASOSVSNNLH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 RASOSISNNIH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (from the glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (from the species: Mus musculus (house mouse)

C, Species: Mus musculus (house mouse)

C, Species: Mus musculus (house mouse)

C, Accession: B45722

R, Simpson, J. A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquan, Vicil 67, 489:496, 1993

A, Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hugherence number: A49722; Mulb:93100833; PMLD:7677958

A, Accession: B45722

A, Antitle: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hugherence number: A49722; Mulb:93100833; PMLD:7677958

A, Antitle: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hugh A, Antitle: preliminary; not compared with conceptual translation

A, Molecule type: nucleic acid
A, Note: sequence extracted from NCBI backbone (NCBIP:120590)
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: glycoprotein
F, 16-90/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cincession: A45722
Risimpson, U.A.; Chow, U.C.; Baker, U.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu, V. Virol. 67, 489-4965, 1993
A; Yirol. 67, 489-4965, 1993
A; Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu A; Reference number: A45722; MUID:93100833; PMID:7677958
A; Accession: A45722
A; Accession: A57722
A; Residual proper mRNA
A; Moslecule type: mRNA
A; Residuas: 1-107 < 4817A
A; Residuas: 1-107 < 4817A
A; Note: sequence extracted from NOBI backbone (NOBIP:120589)
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: glycoprotein
F; 16-90/Domain: immunoglobulin homology < INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - mouse (fra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) C;Species: Mus musculus (house mouse) C;Species: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A26471
Ig kappa chain precursor V region (MAK33) - mouse
C;Species: Mus musculus (house mouse)
C;Date: O5-Jun-1988 #sequence_revision O5-Jun-1988 #text_change 23-Jul-1999
C;Accession: A26471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.4%; Score 42; DB 2; Length 107; Best Local Similarity 72.7%; Pred. No. 0.25; Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                   Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                      2; Indels
                                                                              Score 42; DB 2;
Pred. No. 0.25;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 2;
Pred. No. 0.25;
1; Mismatches
F;13-87/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.4%;
ilarity 72.7%;
Conservative
                                                                                   Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RASOSIGTNIH 11
                                                                                                                                                                                                                                                     1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                    21 RASOSISNNLH 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 RASOSISNNLH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RASOSISNNLH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                     à
```

```
à
                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                          C;Accession: 837511
R;Klein, U.; Kueppers, R.; Rajewsky, K.
Bubmitted to the BMBL Data Library, September 1993
A;Description: Human IgM(*)IgD(*) cells, the major B cell subset in the peripheral blood A;Reference number: 837501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain NIG93 precursor - human
C.Species: Homo sapiens (man)
C.Date: OS-Dec-1998 #sequence_revision OS-Dec-1998 #text_change 21-Jan-2000
C.Accession: UE0243
R.Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
Bubmitted to JIPID, November 1998
A.Description: A new subgroup of K type light chains (VkV) identified in cases of AL amy
A.Reference number: UE0243
                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                Species: Homo sapiens (man)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig Kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-91 «KLE»
A; Cross-references: EMBL.226600; NID:g405664; PIDN:CAA81354.1; PID:g405665
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Accession: $40370 F.; Zachau, H.G.
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:9408091; PMID:8258341
A;Accession: $40370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-215 <ALI.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;I6-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 215;
     Score 40; DB 2; Length 95;
Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 2; Length 91;
Pred. No. 0.89;
2; Mismatches 1; Indels
                                                      1; Indels
                                                                                                                                                                                                                                                                         Ig kappa chain V region (V-kappa 3) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 2
Pred. No. 2.3;
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative 5
Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.9
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                    1 RASOSIGTNIH 11
                                                                                                                                ||||||||::|
24 RASQSIGSFLH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RASOSIGINI 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 RASOSVGNNL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RASOSIGINI 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RASOSVATNV 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S37511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
JE0243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
S40370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
A;Status: preliminary, translation not shown
A;Macule type: mRNA
A;Residues: 1-122 < KLE.
A;Residues: 1-122 < KLE.
A;Residues: 1-122 < KLE.
A;Cross-references: EMBL:X72480; NID:9441428; PIDN:CAA51148.1; PID:9441429
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology c;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
```

# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 16:24:54; Search time 19.4912 Seconds

(without alignments)
29.135 Million cell updates/sec
Title: US-09-635-974A-8
Perfect score: 55
Sequence: 1 RASQSIGTNIH 11
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 38941

389414 seqs, 51625971 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database: Issued\_Patents\_AA:\*
1: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

|              | Description    | Sequence 53, Appl | equence 53        | 53                | 4               | equence 4,   | 4                | Sequence 4, Appli | equence 4, | é,           | œ      | equence 10 | 9            | ώ            | 10,           | 9      | œ        | 10,     | 8       | equence 8, | œ         | ď   | equence 49    | m        | equence 20 | ٠,            | Sequence 1, Appli | Sequence 1, Appli |
|--------------|----------------|-------------------|-------------------|-------------------|-----------------|--------------|------------------|-------------------|------------|--------------|--------|------------|--------------|--------------|---------------|--------|----------|---------|---------|------------|-----------|-----|---------------|----------|------------|---------------|-------------------|-------------------|
|              | QI             |                   | US-08-127-721A-53 | US-08-485-246A-53 | US-08-800-198-4 | -09-296-5    | US-08-476-176B-4 | US-08-127-721A-4  | -246A-     | 08-476-176B- | 8-476- | 08-476-1   | 38-127-721A- | 08-127-721A- | -08-127-721A- | -246A- | -08-485- | -08-485 | -800-19 | -09-296-59 | -08-653-4 | -39 | -07-942-245-4 | 25-539A- | -08-436-   | -08-107-669D- | -08-472-788A-     | US-08-477-531B-1  |
|              | DB             | 7                 | m                 | ٣                 | ~               | m            | 7                | m                 | ო          | 7            | 7      | ~          | ო            | ო            | m             | m      | ო        | ო       | 0       | ო          | N         | (7) | Н             | 4        | Н          | М             | Н                 | N                 |
|              | Length         | 11                | 11                | 11                | 106             | 106          | 107              | 107               | 107        | 127          | 127    | 127        | 127          | 127          | 127           | 127    | 127      | 127     | 240     | 240        | 143       | 240 | 11            | 31       | 107        | 107           | 107               | 107               |
| . <b>a</b> p | Query<br>Match | 100.0             | 100.0             | 100.0             |                 | ٠.           |                  | 100.0             | 100.0      | 100.0        | 100.0  | -          | 100.0        |              |               | 100.0  |          |         |         | 100.0      |           |     | 7             | 7        | ۲.         | 7             | 87.3              | 87.3              |
|              | Score          | 55                | 55                | 55                | 55              | 55           | 55               | 55                | 55         | 55           | 55     | 55         | 55           | 55           | 55            | 55     | 55       | 55      | 55      | 55         | 50        | 50  | 48            | 4.8      | 48         | 48            | 48                | 48                |
|              | Result<br>No.  |                   | 7                 | M                 | 4               | <sub>C</sub> | 9                | 7                 | <b>6</b> 0 | 6            | 10     | 11         | 12           | 13           | 14            | 15     | 16       | 17      | 18      | 19         | 20        | 21  | 22            | 23       | 24         | . 25          | 26                | 27                |

| 44044444HHUUHUHU                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence 19, Appl<br>Sequence 21, Appl |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------|
| -08 -082 -842A-<br>-08 -232 -081B-<br>-08 -232 -081B-<br>-08 -232 -081B-<br>-07 -956 -399 4<br>-08 -326 -399 4<br>-08 -326 -385 -1<br>-08 -472 -087 -2<br>-09 -472 -087 -2 | US-08-436-463-19<br>US-08-436-463-21   |
| 0 1 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                        |                                        |
| 11001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>10                                                                                                                                                                                                                                                                                                                                                                                    | 100                                    |
| 800000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                        | 76.4<br>76.4                           |
| 0 0 0 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7                                                                                                                                                                                                                                                                                                                                                                                                        | 4 4<br>2 2                             |
| и и и и и и и и и и и и и и и и и и и                                                                                                                                                                                                                                                                                                                                                                                                          | 44<br>45                               |

# ALIGNMENTS

| •                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Gaps                                                                                                                                                    |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|
| ជ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ,,                                                                                                                                                      |
| Application US/08476176B 5558708 FORMATION: T: Hardman, No. 5958708man T: Hardman, Jose T: Raldanha, Jose T: Reshaped monoclonal antibodies against T: Saldanha, Jose T: Reshaped monoclonal antibodies against T: Saldanha, Jose TINVENTION: Reshaped monoclonal antibodies against TINVENTION: Immunoglobulin isotype Rest ENDERS. 558708artis Patent Department Respublic FORM: New Jersey T: USA NEADABLE FORM: TYPE: Floppy disk ER: IBM PC compatible ER: SEPERM: PC-DOS/MS-DOS RE: PatentIn Release #1.0, Version #1.25 APIDION NUMBER: US/08/476,176 DATE: 27-SEPTEMBER: 1992 APIDION NUMBER: US 07/952,802 DATE: 25-SEPTEMBER-1993 APIDN NUMBER: US 07/952,802 DATE: 25-SEPTEMBER-1992 APIDN NUMBER: US 07/952,802 DATE: 25-SEPTEMBER-1992 APIDN NUMBER: US 07/952,802 DATE: 25-SEPTEMBER-1992 APIDN NUMBER: US 07/952,802 DATE: 27-4306 APIDN NUMBER: US 07/952,802 APIDN NUMBER: US | Query Match 100.0%; Score 55; DB 2; Length 11;<br>Best Local Similarity 100.0%; Pred. No. 0.0001;<br>Matches 11; Conservative 0; Mismatches 0; Indels ( |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                         |

ö

Thu Oct 14 09:37:01 2004

g

q

```
Sequence 4, Application US/08800198
Patent No. 5942602
GENERAL INFORMATION:
APPLICANT: WELS, WINFRIED S.
APPLICANT: SCHNIDT, MATHIAS
APPLICANT: SCHNIDT, MOUGLAS
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORPOTER READALE FORM:
COMPUTER READALE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPILCATION NUMBER: US/08/800,198
FILING DATE: 13-FEB-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C. 12200 CLARENDON BLVD. SUITE 1400 ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (908) 277-5110
                                            STATE: New Jersey
COUNTRY: USA
ZIP: 07936-108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RASQSIGTNIH 11
59 Route 10
                            East Hanover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
STREET: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-485-246A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-800-198-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-485-246A-53
US-08-485-246A-53
Sequence 53, Application US/08485246A
Sequence 53, Application US/08485246A
Septement No. 6072035
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SECUENCES: 55
CONTRESPONDENCE ADDRESS:
ADDRESSEE: No. 6072035artis Patent Department
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6066718artis Patent and Trademark Department
STREET: 59 Route 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 55; DB 3; Length 11; 100.0%; Pred. No. 0.0001; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION TAX:

APPLICATION NUMBER: U8 07/952,802

FILING DATE:

APPLICATION NUMBER: U8 07/952,802

FILING DATE:

APPLICATION NUMBER: U8 07/952,802

ATONNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 33,200

REFERENCE/COCKET NUMBER: 4-19276/A/P2/CIP

TELECOMMULCATION INFORMATION:

TELEPHONE: (908) 277-5110

TELEPHONE: (908) 277-510

TELEPHONE: (908) 277-4306

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:
                                                                                                                                          RESULT 2
US-08-127-721A-53
F. Sequence 53, Application US/08127721A
Patent No. 6066718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 11 amino acids
                       RASOSIGINIH 11
                                                                   1 RASOSIGTNIH 11
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 55; DB 3; Length 11; 100.0%; Pred. No. 0.0001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: Patentin Release #1.0, Version #1.25
SOUTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
FILING DATE: US/08/485,246A
FILING APPLICATION NUMBER: US/08/485,246A
FILING APPLICATION NUMBER: US/07/721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US/07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGBNT INPORMATION:
NAME: NO. 6072035ak, Henry P.
REGISTRATION NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INPERE: 4-19276/A/P2/CIP
TELECOMMUNICATION INPERE: 4-19276/A/P2/CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
```

```
RESULT 7
US-08-127-721A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-476-176B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pactor of Application US/08476176B

pactor No. 5958708

GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Rolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: Remanaglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STREET: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 55; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 55; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09296595A

Patent No. 6129915

GRUERAL INFORMATION

APPLICANT: WELS, WINFRIED S.
APPLICANT: VAKALOFOLLOU, EVANGELIA

APPLICANT: VAKALOFOLLOU, EVANGELIA

APPLICANT: SCHNIDER, DOUGLAS

TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES

TITLE OF INVENTION OF BROWTH FACTOR RECEPTOR ANTIBODIES

CURRENT APPLICATION NUMBER: US/09/296,595A

CURRENT PILICATION NUMBER: 08/800,198

EARLIER RILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 106
REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEPAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS;
                                                                                                                                             LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                      . peptide
NO
                                                                                                                                                                                                                                                                                          internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 RASQSIGTNIH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 RASOSIGINIH 34
                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: pepti
HYPOTHETICAL: NO
FRAGMENT TYPE: inter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
; ORGANISM: Murine sp.
US-09-296-595-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-476-176B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-296-595-4
                                                                                                                                                                                                                                                                                                              US-08-800-198-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
12. COMPUTER READMALE FORM:

MORDING THESE INDEPT BROADMALE FORM:

MORDING THESE INDEPT BROADMALE FORM:

MORDING THESE INDEPT BROADMALE THE MORDING THE LINES THE MORDING THE
```

```
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION WINMER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5982708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/
TELEPHONE: (908) 277-5110
TELEPAX: (908) 277-5110
                                                                                                  Sequence 6, Application US/08476176B Patent No. 5958708
                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity luv.
Pest Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: protein
24 RASQSIGTNIH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 RASOSIGINIH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                  US-08-476-176B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-08-476-176B-8
                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08485246A
Patent No. 6072035
GENERAL INPORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6072035artis Patent Department
STREET: 59 Route 10
                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                 Query Match 100.0%; Score 55; DB 3; Length 107; Best Local Similarity 100.0%; Pred. No. 0.0012; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 55; DB 3; Length 107; Best Local Similarity 100.0%; Pred. No. 0.0012; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4-19276/A/P2/CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424

PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER:1993
APPLICATION NUMBER: 07/952,802
FILING DATE: 25-SEPTEMBER:1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,20
REFENCE/DOCKET NUMBER: 4-19276/A/P:
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-510
TELEPAX: (908) 277-510
TELEPX: (908) 277-510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELECOMMUNICATION INFORMATION
               TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                         : 107 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 107 amino acids
amino acid
                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-127-721A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                    1 RASOSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                            24 RASOSIGINIH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 59 ROLLS
CITY: Bast Hanover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-485-246A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-485-246A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
```

1 RASQSIGTNIH 11

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08476176B
Patent No. 5958708
GENERAL INFORMATION:
APPLICANT: Rolbinger, Frank
APPLICANT: Rolbinger, Frank
APPLICANT: Rolbinger, Frank
APPLICANT: Rolbinger, Reshaped monoclonal antibodies against an TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSS:
ADDRESSEE: No. 5958708artis Patent Department
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: immunoglobulin isotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 55; DB 2; Length 127; 100.0%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PALENTEN: PC-DOS/MS-DOS SOFTWARE: PALENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/476,176B
                                                                                                                      NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS: ADDRESSEB: ADDRESSEB: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: No. 40589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08127721A
| Patent No. 6066718
| GENERAL INFORMATION:
| APPLICANT: Hardman, No. 6066718man
| APPLICANT: Kolbinger, Frank
| APPLICANT: Saldanha, Jose
| TILLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: Immunoglobulin isotype
| NUMBER OF SEQUENCES: 55
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: No. 6066718artis Patent and Trademark Department STRET: 59 Route 10 CITY: Bast Hanover STATE: New Jersey COUNTRY: USA ZITE: New Jersey COUNTRY: USA ZITE: 07936-1080 COMPUTER READABLE FORM: MEDIUM TYPE: IBM PC COMPUTER: IBM PC COMPUTER: OPSERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Score 55; DB 2; Length 127; Pred. No. 0.0015; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

100.0%; Score 55; DB 3; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE PATENTIN STILL SOFTWARE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: S-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6066718ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708 ak, Henry P.
REGISTRATION NUMBER: 33,200
REGISTRANGE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-510
INPORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (908) 277-5110
                                                                                                                                                                                                                                                                                                                                    127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 127 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-476-1768-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-127-721A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 RASOSIGTNIH 54
                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08476176B
Sequence 10, Application US/08476176B
Setent No. 5958708
GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Hardman, No. 5958708man
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Immunoglobulin isotype
TITLE OF INVENTION: immunoglobulin isotype
TITLE OF INVENTION: immunoglobulin isotype
SEQUENCES:
ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
CONPUTRY: USA
COMPUTRY: USA
COMPUTRY: USA
COMPUTRY: ISM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
PRINT DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 100.0%; Score 55; DB 2; Length 127; Best Local Similarity 100.0%; Pred. No. 0.0015; Matches 11; Conservative 0; Mismatches 0; Indels
                                                       COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: 08 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REPERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPRAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 127 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-476-176B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RASQSIGTNIH 11
East Hanover
New Jersey
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-476-176B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH:
```

qq à

ö

```
T: 59 Route 10
East Hanover
: New Jersey
                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-08-485-246A-6
   STREET:
CITY: Ea
STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1 SEGUENCES: 5 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6066718artis Patent and Trademark Department STREET: 5 Route 10
CITY: East Hanover STATE: New Jereey
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: 1BM PC compatible
COMPUTE
                                                                                                                                                                                                                                                                         Sequence 8, Application US/08127721A
Patent No. 6066718
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Ralbinger, Frank
APPLICANT: Raldman, Ose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08127721A

Sequence 10, Application US/08127721A

Patent No. 6066718

GRDERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Saldanha, 108e
TITLE OF INVENTION: immunoglobulin isotype
TITLE OF INVENTION: immunoglobulin isotype
COURESPONDENCE ASS:
CORRESPONDENCE ASS:
CORRESPONDENCE No. 6066718artis Patent and Trademark Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 55; DB 3; Length 127; 100.0%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 127 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                    1 RASOSIGINIH 11
                                                                                       44 RASQSIGTNIH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RASQSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 RASQSIGTNIH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-127-721A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-127-721A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                           ઠે
                                                                                                         ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

```
GTTY: EAR HARDOWER

GTTY: Read HARDOWER

GONNEY: New Jorge

CONNING: WEADOW GIAN

COMPUTER: IN TO COMPATIBLE

FILING DATE: 27-28FERBER-1992

FILING DATE: 27-28FERBER-1992

FILING DATE: 27-28FERBER-1992

FILING DATE: 37-28FERBER-1992

FILING DATE: 37-28FERBER-1992

FILING DATE: NAME: 33-200

FILING DATE: 37-28FERBER-1992

FILING DATE: NAME: 33-200

FILING DATE: NAME: 33-200

FILING DATE: 37-28FERBER-1992

FILING DATE: NAME: 33-200

FILING DATE: 37-28FERBER-1992

APPLICANT: SOLIDIGE: PEAR

FILING DATE: 39-28FERBER-1992

CONDUMER: 28-28FERBER-1993

CONDUMER: 28-28FERBER-1993

FILING DATE: 28-28FERBER-1993

FILING DATE: 37-28FERBER-1993

FILING DATE: 3
```

.; 0

OM protein - protein search, using sw model

October 6, 2004, 16:20:48 ; Search time 55:5789 Seconds (without alignments) 55.921 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-635-974A-8 55 1 RASQSIGTNIH 11

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* A\_Geneseq\_29Jan04:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |        | Description  | Aay26990 CDR1 doma | 4        | Ŋ        | _        | 41 Light | Light    |          | 8 Карра    | 9 Light  | 4        | 192 Light c | Aar50187 Light cha |          |          | 1 Kappa  | Aaw08946 Kappa lig | Aaw08943 Kappa lig | Aay26981 Light cha | Light |          | 33       | 43 SCF   | SCF      | Aaw05135 scFv(225) | Aaw05140 scFv2(225 |
|-----------|--------|--------------|--------------------|----------|----------|----------|----------|----------|----------|------------|----------|----------|-------------|--------------------|----------|----------|----------|--------------------|--------------------|--------------------|-------|----------|----------|----------|----------|--------------------|--------------------|
| SUMMARIES | ţ      | di<br>di     | AAY26990           | AAY59314 | AAB37955 | AAU77787 | AAW71241 | AAR50190 | AAW08949 | AAW08948   | AAY26979 | AAY70604 | AAR50192    | AAR50187           | AAR50191 | AAW08945 | AAW08941 | AAW08946           | AAW08943           | AAY26981           | æ     | AAY26982 | AAW05133 | AAW71243 | AAY70605 | ᄗ                  | AAW05140           |
|           | í      | DBC          | 0                  | m        | 4        | Ŋ        | ~        | ~1       | 7        | 7          | N        | m        | ~           | ~1                 | 0        | 7        | 7        | 7                  | ~                  | ~                  | ~     | Ŋ        | Ŋ        | Ŋ        | m        | α                  | 0                  |
|           | 1      | Match Length | 11                 | 11       | 11       | 11       | 106      | 107      | 107      | 107        | 107      | 107      | 127         | 127                | 127      | 127      | 127      | 127                | 127                | 127                | 127   | 127      | 240      | 240      | 245      | 651                | 892                |
| ₩         | Query  | March        | 100.0              | 100.0    | 100.0    | 100.0    | 100.0    |          | 00       | 8          | 100.0    | 100.0    | 100.0       | 100.0              | 100.0    | 100.0    | 100.0    | 100.0              | 100.0              | 100.0              | 100.0 | 100.0    | 100.0    | 100.0    |          | 100.0              | 100.0              |
|           |        | score        | r.                 | 52       | 52       | ເນ       | . 25     | ວ        | ភ<br>ស   | 55         | ວ        | សួ       | 52          | 52                 | 52       | 52       | 55       | 52                 | 52                 | 22                 | 52    | 52       | S<br>S   | ខេ       | ນ        | 55                 | 55                 |
|           | Result | . 02         | н                  | 7        | ю        | 4        | ស        | ø        | 7        | <b>c</b> o | O        | 10       | 11          | 12                 | 13       | 14       | 15       | 16                 | 17                 | 18                 | 13    | 20       | 21       | 22       | 23       | 24                 | 25                 |

| 39 SCFV2 (FRP<br>41 SCFV2 (FRP<br>51 Monoclona<br>52 Anti-TL2R<br>50 Anti-TL2R<br>50 Anti-TL2R<br>6 Monoclona<br>80 Mouse ant<br>57 TSH recep<br>67 TSH recep<br>67 TSH recep<br>67 TSH recep<br>61 TSH recep<br>62 TSH recep<br>62 TSH recep<br>63 TSH recep<br>64 TSH recep<br>65 TSH recep<br>65 TSH recep<br>66 TSH recep<br>67 TSH recep<br>68 TSH recep<br>68 TSH recep<br>69 TSH recep<br>61 TSH recep<br>61 TSH recep<br>62 TSH recep<br>63 TSH recep<br>64 TSH recep<br>65 TSH recep<br>65 TSH recep<br>66 TSH recep<br>67 TSH recep<br>68 TSH recep<br>68 TSH recep<br>69 TSH recep<br>61 TSH recep<br>63 TSH recep<br>64 TSH recep<br>65 TSH recep<br>65 TSH recep<br>66 TSH recep<br>67 TSH recep<br>68 TSH recep<br>68 TSH recep<br>68 TSH recep<br>69 TSH recep<br>61 TSH recep<br>61 TSH recep<br>63 TSH recep<br>64 TSH recep<br>65 TSH recep<br>65 TSH recep<br>66 TSH recep<br>67 TSH recep<br>68 TSH recep<br>68 TSH recep<br>68 TSH recep<br>69 TSH recep<br>61 TSH recep<br>61 TSH recep<br>61 TSH recep<br>63 TSH recep<br>64 TSH recep<br>65 TSH recep<br>65 TSH recep<br>66 TSH recep<br>67 TSH recep<br>68 T | 23 H. pylori<br>09 H. pylori               |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------|
| Aaw05139 Aaw05141 Aaw45141 Aaw428518 Aar32129 Aaw19580 Abp96766                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Aab1002<br>Aab8610                         |
| AAW05139 AAW05141 AAW0514178 AAU72851 AAR32129 AAW14176 AAW19580 AAW19580 AAW19580 AAW19580 AABP96756 ABP96756 ABP96766 ABP96765 AABP96766 AABP96766 AABP96766                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | AAB10023<br>AAB86109                       |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | . w 4                                      |
| 892<br>1020<br>111<br>111<br>107<br>1107<br>1107<br>1107<br>1107<br>1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 107                                        |
| 11<br>900000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 8 8 8<br>1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 |
| N N N N N N N N N N N N N N N N N N N                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | . 4. 4.<br>10. 0                           |
| G G G G E E E E E E E E E E E E E E E E                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 44                                         |

# ALIGNMENTS

RESULT 1

Diagnosis; IgE; immunoglobulin; body fluid; human; monoclonal antibody; binding affinity; mouse; CDR; complementarity determining region; CDR1 domain reshaped human antibody light chain variable region. AAY26990 standard; protein; 11 AA. 24-DEC-1999 (first entry) AAY26990; allergy. **AAY2699**0 

Synthetic. Homo sapiens.

95US-00476176. 07-JUN-1995; US5958708-A. 28-SEP-1999

(NOVS ) NOVARTIS CORP. (TANO-) TANOX BIOSYSTEMS INC. 92US-00952802. 93US-00127721. 25-SEP-1992; 27-SEP-1993;

Saldanha J, Kolbinger F, Hardman N; WPI; 1999-570765/48. new method for determining IgE levels in a sample.

Claim 5; Col 67; 19pp; English.

The invention relates to a method of determining IgE levels in a body fluid sample, by contacting the sample with a reshaped human monoclonal antibody (RA) having a binding affinity about equal to that of the murine CDR-donor antibody TES-C21 produced by the cell line 11133. The antibodies are useful in the diagnosis, prophylaxis and treatment of allergy. This sequence represents the complementarity determining region (CDR) 1 from the light chain variable domain of a reshaped human antibody

Query Match

100.0%; Score 55; DB 2; Length 11;

Ŋ

```
Refractory tumour growth inhibition; epidermal growth factor receptor; EGFR antagoniet; cancer; squamous cell carcinoma; anti-EGFR antibody; complementarity determining region; CDR.
                                               Anti-EGFR monoclonal antibody L chain V region CDR1 peptide sequence.
                                                                                                                                                                                             01-MAY-2000; 2000WO-US011756.
                                                                                                                                                                                                                                                        IMCL-) IMCLONE SYSTEMS INC
                       12-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                         WPI; 2001-016160/02.
                                                                                                                                               WO200069459-A1
                                                                                                                                                                                                                      14-MAY-1999;
                                                                                                                                                                                                                                  13-AUG-1999;
                                                                                                                                                                       23-NOV-2000
                                                                                                                                                                                                                                                                                  Waksal HW;
AAB37955;
                                                                                                                         Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the hypervariable region CDR1 (complementarity determining region 1) of the light chain of a single chain antibody derived from the murine antibody 225. The invention relates to a method for inhibiting the growth of tumours in human patients by treating with an effective amount of a combination of radiation and a non-radiolabelled protein receptor tyrosine kinase (PRTK) inhibitor, the overexpression of which can lead to tumourigenesis. The method can be used in the treatment of tumours of e.g. breast, lung, colon, kidney, bladder, head and neck, ovary, prostate or brain. The administration of a suitable antibody to the patient makes the tumour more susceptible to radiotherapy
                                                                                                                                                                                                                     Hypervariable region; complementarity determining region; CDR; tumour; single chain antibody; growth inhibitor; human; tumourigenesis; therapy; protein receptor tyrosine kinase; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of human tumors, using a combination of radiation and a non-radiolabeled protein receptor tyrosine kinase inhibitor.
               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 55; DB 3; Length 11; 100.0%; Pred. No. 0.00023; ive. 0; Mismatches 0; Indels
               0; Indels
  Pred. No. 0.00023;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buchsbaum DJ;
                                                                                                                                                                                                Light chain hypervariable region, CDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 15; 31pp; English.
                                                                                                                           AAY59314 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robert F,
               ;
0
   100.001
                                                                                                                                                                                                                                                                                                                                                                      98US-00079612.
                                                                                                                                                                                                                                                                                                                                                99WO-US010741,
                                                                                                                                                                                                                                                                                                                                                                                  98US-0085613P.
98US-00206138
                                                                                                                                                                                                                                                                                                                                                                                                                      (IMCL-) IMCLONE SYSTEMS INC (UABR-) UAB RES FOUND.
                                                                                                                                                                         07-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 11, Conservative
               Conservative
                                        RASOSIGINIH 11
                                                              RASOSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saleh MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-062440/05.
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ48628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11 AA;
                                                                                                                                                                                                                                                                                                WO9960023-A1
                                                                                                                                                                                                                                                                                                                                               14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                        15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                  15-MAY-1998;
                                                                                                                                                                                                                                                                                                                        25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HM,
                                                                                                                                                  AAY59314;
                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waksal
                                                                                                            ò
                                                              d
```

99US-00312284. 99US-00374028.

```
This invention relates to a method for inhibiting the growth of refractory tumours that are stimulated by a ligand of epidernal growth factorized to receptor (EGFR) in human patients. The method involves treating the patient with a combination of EGFR/Human EGF-1 (HER1) antegonist, optionally with a chemotherapeutic agent or radiation. The antagonist can be for example a chimeric anti-EGFR monoclonal antibody, C225. The CC EGFR/HER1 antagonist is useful for inhibiting the growth of refractory tumours such as tumours of breast, heart, lung, small intestine, colon, Eplem, kidney, bladder, head and heart, ovary, prostate, brain, pancreas, skin, bone, bone marrow, blood, thymus, uterus, testicles, cervix and liver, preferably squamous cell carcinomas. The present sequence region complementarity determining region 1 amino acid sequence of the chimeric anti-EGFR monoclonal antibody C225 which is used in an example illustrating the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                               Epidermal growth factor receptor/human epidermal growth factor receptor-1 antagonist for inhibiting the growth of refractory tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse, light chain, antibody, hyperproliferative disease, epidermal growth factor, EGF, psoriasis, actinic keratosis, seborrheic keratosis, warts, keloid scars, eczema, 255 antibody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse light chain hypervariable region (CDR1) of 225 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Match 100.0%; Score 55; DB 4; I
Local Similarity 100.0%; Pred. No. 0.00023;
Les 11; Conservative 0; Mismatches 0;
                                                                                                                                            Disclosure, Page 14, 31pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU77787 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RASOSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RASOSIGINIH 11
N-PSDB; AAC83238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU77787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU77787
```

.. 0

Gaps . 0

AAB37955 standard; protein; 11 AA.

RESULT 3
AAB37955
ID AAB3

1 RASOSIGINIH 11 RASOSIGTNIH 11

Mus sp.

```
New single chain polypeptide that binds to epidermal growth factor receptor - is derived from antibody 14E, used for treatment and diagnosis of cancer or other cell proliferative diseases.
                                                                                                                                                                                                                                                                                                                                    The present sequence represents the light chain variable domain of murine monoclonal antibody 14E1. This antibody is active against the human epidermal growth factor receptor (EGF-R). The sequence is used to construct a single-chain polypeptide (scFv) that has binding affinity for an EGF-R. The scFv comprises two segments which contain the binding parts of the heavy and light chain variable domains of the monoclonal antibody 14E1. The scFvs of the invention used to cardinomas (gliomas, melanomas and tumours) that overexpress EGF-R, specifically EGF-RVIII, relative to normal cells, particularly by blocking proliferation of such vitro purging. When the scFv is appropriately labelled, it can be used diagnostically to image cells that express EGF-R, specifically breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody; heavy chain; light chain; variable region; therapy; constant region; prophylaxis; prevention; allergy; identification; allergic reaction; immunoglobulin; IgE; determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 55; DB 2; Length 106; 100.0%; Pred. No. 0.0031; ive 0; Mismatches 0; Indels
                                                                                                          Schneider DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Light chain variable region of TES-C21 antibody.
                                                                                                          Vakalopoulou E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR50190 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                   Example 1; Fig 11D; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50. .56
/label= CDR 2.
89. 97
/label= CDR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDR 1.
                        97US-00800198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93EP-00810653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92GB-00020228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
---nhas 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24. .34
/label= (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RASOSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 RASQSIGTNIH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003 (revised)
18-OCT-1994 (first en
                                                                                                        Schmidt M,
                                                                                                                                                  WPI; 1998-467176/40.
                                                                  (SCHD ) SCHERING AG.
                                                                                                                                                                         N-PSDB; AAV54788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 106 AA;
                      13-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP589840-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR50190;
                                                                                                        Wels WS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a novel method for treating a mammal with the hyperproliferative disease stimulated by a ligand of a member of the epidermal growth factor (BGF) family of receptors. The method involves caministering an antibody or a defective receptor that is an antagonist of a member of the EGF receptor family, or a combination of the antagonist and phototherapy, chemotherapeutic agent or radiation therapy. The antibody used in the method of the invention acts as an epidermal growth factor receptor (BGFR) antagonist by inhibiting EGFR /HERL phosphorylation. The method of the invention is useful for treating a mammal with hyperproliferative disease such as psoriasis, actinic keratoses, seborrheic keratoses, wartes, keloid scars and eczema stimulated by a ligand of a member of the EGF family of receptor. This sequence represents the murine anti-EGF 255 antibody light chain (LH) the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                Treating a mammal with hyperproliferative disease especially psoriasis, stimulated by ligand of member of epidermal growth factor family of receptors, by administering antagonist of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Light chain variable domain; antibody 14E1;
human epidermal growth factor receptor; EGF-R; treatment; carcinoma;
EGF-RvIII; in vitro purging; breast carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 55; DB 5; Length 11; Best Local Similarity 100.0%; Pred. No. 0.00023; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Light chain variable domain of antibody 14E1.
hypervariable region; CDR1; EGFR inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW71241 standard; protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 12; 28pp; English.
                                                                                                                                                                                                            09-AUG-2000; 2000US-00635974.
                                                                                                                                                                  09-AUG-2001; 2001WO-US041647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-IB000413
                                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RASOSIGINIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RASOSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                      WPI; 2002-257423/30.
N-PSDB; ABK11443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11 AA;
                                                                                  WO200211677-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9836074-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-1998;
                                                                                                                          14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW71241;
```

Mus sp

RESULT 5 AAW71241

g ઠ

ö

Gaps

;

Saldanha JW;

```
Kappa, light chain, reshaped, monoclonal; antibody; 225RA; human; cell; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                               Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                             The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RKA. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytocoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 2; Length 107; 100.0%; Pred. No. 0.0032; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kappa light chain variable region of 225RA antibody.
                                                                                                                                                           Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57. 88
/label= framework_3
89. 97
/label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15. .49
'label= framework_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98. .107
/label= framework_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .23
label= framework_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW08948 standard; protein; 107 AA.
                                                                                                                                                                                                                                                       Claim 29; Fig 21; 112pp; English
                                                                                                                   (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50. .56
/label= CDR_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24. 34
/label= CDR_1
                                                96WO-US009847.
                                                                            95US-00482982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RASOSIGINIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 RASOSIGINIH 34
                                                                                                                                                                                      WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 107 AA;
                                                   07-JUN-1996;
                                                                            07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
WO9640210-A1
                        19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW08948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kappa; light chain; reshaped; monoclonal; antibody; 225RB; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                          Reshaped human monoclonal antibodies can be used in the prophylaxis and/or treatment of allergic reactions in humans. The monoclonal antibodies can also be used for the qualitative or quantitative determination of IgE and for the determination of surface IgE positive B cells. They can provide a long lasting therapeutic effect without inducing immunogenicity as foreign proteins. The CDK's from the variable heavy and light chains of the murine antibody TES-C21 were used in the construction of a molecular model of the variable heavy and light chains of a human reshaped antibody which also comprised human variable heavy and light chain framework regions. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                             New reshaped human monoclonal antibody specific for IgE - used for prophylaxis or treatment of allergic reactions or qualitative or quantitative determn. of IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                       'Match 100.0%; Score 55; DB 2; Length 107; Local Similarity 100.0%; Pred. No. 0.0032; les 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kappa light chain variable region of 225RB antibody.
                                                                               Hardman N, Kolbinger F, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50. .56
/label= CDR_2
57. 88
/label= framework_3
89. 97
/label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98. .107 _ // label= framework_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5. .49 __label= framework_2
                                                                                                                                                                                                     Disclosure; Page 28; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .23
/label= framework 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW08949 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4. .34
/label= CDR_1
                        (CIBA ) CIBA GEIGY AG.
(TANO-) TANOX BIOSYSTEMS INC.
(NOVS ) NOVARTIS AG.
92US-00952802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RASOSIGINIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 RASOSIGINIH 34
                                                                                                         WPI; 1994-103410/13.
                                                                                                                     N-PSDB; AA044714
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 107 AA;
25-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW08949;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

0

Gaps

. 0

(MRCC-)

```
The invention relates to a method of determining IgE levels in a body fluid sample, by contacting the sample with a reshaped human monoclonal antibody (RA) having a binding affinity about equal to that of the murine CDR-donor antibody TES-C21 produced by the cell line 11133. The antibodies are useful in the diagnosis, prophylaxis and treatment of allergy. This sequence represents the light chain variable domain from the TES-C21 antibody. The fragments encoding the complementarity determining regions are used to generate the reshaped antibodies of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present protein sequence is the Vkappa (kappa chain variable region) of the humanised antibody Hu-901. This is an exemplary anti-1gE (anti-immunoglobulin E) monoclonal antibody produced by hybridoma TES-C21. The heavy and light chains are obtained through RT-PCR using the RNA from the transfectorian cell line producing the chimeric antibody. Humanised anti-IEB genes are incorporated in the genome of a recombinant adenovirus vector as an independent transcriptional unit, and packaged into infections virus particles. Upon infection of host, the recombinant adenovirus vector will direct the production of either intext anti-IgE antibody or an scFv fragment in the serum, which will bind free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised antibody-901, Hu-901; Vkappa; kappa chain variable region; anti-19g; anti-1egional antibody; hybridoma TES-C21; recombinant adenovirus vector; anti-19g antibody; gene therapy; scFv; single chain variable fragment; allergy; antiallergic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids encoding anti-IgE antibodies such as Hu-901 or their fragments, useful in the gene therapy of allergic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 55; DB 2; Length 107; 100.0%; Pred. No. 0.0032; ive 0; Mismatches 0; Indels
for determining IgE levels in a sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vkappa region of humanised antibody Hu-901.
                                                             Disclosure; Col 35-36; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY70604 standard; protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 47; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US021646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0100639P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RASOSIGTNIH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 RASOSIGINIH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-271264/23.
N-PSDB; AAZ52078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thomas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TANO-) TANOX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200015260-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                           invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY70604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liou RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
         new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY70604
AAY
   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosis; IgE; immunoglobulin; body fluid; human; monoclonal antibody; binding affinity; mouse; CDR; complementarity determining region; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the kappa light chain variable region of the reshaped human enoclonal antibody (Wab) H225. 225RA, The Mab is specific for the human epidermal growth factor (EGF) receptor. The Mab, or a fragment, can be used to inhibit the growth of tumour cells especially late stage prostatic tumour cells in humans, optionally conjugated to a cytocoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-EGF receptor antibody 225 of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 2; Length 107; 100.0%; Pred. No. 0.0032; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Light chain variable domain from antibody TES-C21.
                                                                                                                                                                                                                                                                                                                                                                        Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hardman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for inhibiting tumour growth, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY26979 standard; protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and humanised versions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 29; Fig 21; 112pp; English.
                                                                                                                                                                                                                                                                                IMCLONE SYSTEMS INC.
MRC COLLABORATIVE CENT
                                                                                                                           96WO-US009847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-00476176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-00952802.
                                                                                                                                                                                     95US-00482982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TANO-) TANOX BIOSYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saldanha J, Kolbinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 RASOSIGTNIH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NOVS ) NOVARTIS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RASOSIGINIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-570765/48.
N-PSDB; AAZ28545.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                           Goldstein NI,
         WO9640210-A1
                                                                                                                              07-JUN-1996;
                                                                                                                                                                                     07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-1992;
27-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5958708-A.
                                                             19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-1999
                                                                                                                                                                                                                                                                             (IMCI-)
```

RESULT 9 AAY26979

g

8

Mus sp

ω

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reshaped human monoclonal antibodies can be used in the prophylaxis and/or treatment of allergic reactions in humans. The monoclonal antibodies can also be used for the qualitative or quantitative determination of IgS and for the determination of surface IgS positive B cells. They can provide a long lasting therapeutic effect without inducing immunogenicity as foreagn proteins. This sequence is a slightly modified version of C21-L1 described in ARE50187, having glutamic acid at position 1 of the mature protein instead of aspartic acid and value at
circulating IgE, resulting in the reduction of free serum IgE. The binding of the antibody or fragment to IgE-bearing B cells may lower IgE levels by down-regulating IgE production by these B cells. These methods are useful in the gene therapy of allergic diseases
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New reshaped human monoclonal antibody specific for IgE - used for prophylaxis or treatment of allergic reactions or qualitative or quantitative determn. of IgE.
                                                                                                                                                                                                                                                                                                                                                                                                Antibody, heavy chain, light chain, variable region, therapy, constant region, prophylaxis, prevention, allergy, identification, allergic reaction, immunoglobulin, IgE, determination.
                                                                                                                                 ;
                                                                                                  100.0%; Score 55; DB 3; Length 10
100.0%; Pred. No. 0.0032;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                     Light chain variable region C21-L3 of reshaped antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                AAR50192 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 36; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70. 76
/label= CDR 2.
109. .117
/label= CDR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44. .54
/label= CDR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92GB-00020228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CIBA ) CIBA GEIGY AG.
(TANO-) TANOX BIOSYSTEMS INC.
(NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93EP-00810653
                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   œ,
                                                                                                                                 11; Conservative
                                                                                                                                                           1 RASQSIGTNIH 11
                                                                                                                                                                                         24 RASOSIGINIH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kolbinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-103410/13.
                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ44716.
                                                                         Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-1992;
25-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-1993;
                                                                                                                                                                                                                                                                                                                          25-MAR-2003
18-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP589840-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1994,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hardman N,
                                                                                                                                                                                                                                                                                              AAR50192;
                                                                                                                                 Matches
                                                                                                                                                                                                                                                 RESULT 11
 8886666
```

```
..
0
  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reshaped human monoclonal antibodies can be used in the prophylaxis and/or treatment of allergic reactions in humans. The monoclonal antibodies can also be used for the qualitative or quantitative determination of IgE and for the determination of surface IgE positive cells. They can provide a long lasting therapeutic effect without inducing immunogenicity as foreign proteins. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
position 3 of the mature protein instead of leucine (positions 21 and respectively of this sequence). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                      Antibody; heavy chain; light chain; variable region; therapy; constant region; prophylaxis; prevention; allergy; identification; allergic reaction; immunoglobulin; IgE; determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New reshaped human monoclonal antibody specific for IgE - used for prophylaxis or treatment of allergic reactions or qualitative or
                                                                                                          ..
                                                                                  Length 127;
                                                                               100.0%; Score 55; DB 2; Length 12
100.0%; Pred. No. 0.0039;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               Light chain variable region C21-L1 of reshaped antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hardman N, Kolbinger F, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
44. .54
/label= CDR 1.
                                                                                                                                                                                                                                  AAR50187 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 29-30; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70. .76
/label= CDR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109. .117
/label= CDR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CIBA ) CIBA GEIGY AG.
(TANO-) TANOX BIOSYSTEMS INC.
(NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93EP-00810653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92GB-00020228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quantitative determn. of IgE.
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                          11; Conservative
                                                                                                                                                              54
                                                                                                                                      1 RASOSIGTNIH 11
                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                              44 RASOSIGTNIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-103410/13.
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ44711
                                                     Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-SEP-1992;
25-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binding-site
                                                                                                                                                                                                                                                                                      25-MAR-2003
                                                                                                                                                                                                                                                                                                   18-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP589840-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAR-1994
                                                                                                                                                                                                                                                              AAR50187;
                                                                                                         Matches
                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                       AAR50187
  88888
                                                                                                                                                             셤
```

Gaps 0

Pred. No. 0.0039; Mismatches 0; Indels

```
Best Local Similarity 100.
Matches 11; Conservative
                                          ò
                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reshaped human monoclonal antibodies can be used in the prophylaxis and/or treatment of allergic reactions in humans. The monoclonal antibodies can also be used for the qualitative or quantitative determination of IgE and for the determination of surface IgE positive B cells. They can provide a long lasting therapeutic effect without inducing immunogenicity as foreign proteins. This sequence is a slightly modified version of C21-L1 described in AAR50187, having aspartic acid at position 60 of the mature protein (position 80 of this sequence) instead of serine. (Updated on 25-MAR-2003 to correct PM field.) (Updated on 25-MAR-2003 to correct PM field.)
                                          Gaps
                                                                                                                                                                                                                                                                                            Antibody; heavy chain; light chain; variable region; therapy; constant region; prophylaxis; prevention; allergy; identification; allergic reaction; immunoglobulin; IgE; determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New reshaped human monoclonal antibody specific for IgB - used for prophylaxis or treatment of allergic reactions or qualitative or quantitative determn. of IgE.
                                         .
           100.0%; Score 55; DB 2; Length 127; 100.0%; Pred. No. 0.0039; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                   Light chain variable region C21-L2 of reshaped antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
44. 54
71 abel= CDR 1.
70. 76
71 abel= CDR 2.
71 abel= CDR 3.
71 abel= CDR 3.
                                                                                                                                                                   AAR50191 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 33; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CIBA ) CIBA GELGY AG.
(TANO-) TANOX BIOSYSTEMS INC.
(NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92GB-00020228
92US-00952802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93EP-00810653
                                                                                                                                                                                                                        (revised)
(first entry)
    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kolbinger F,
                                                                    1 RASQSIGTNIH 11
                                                                                             44 RASQSIGTNIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-103410/13.
N-PSDB; AAQ44715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                              Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                       Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP589840-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1994.
                                                                                                                                                                                                                        25-MAR-2003
18-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hardman N,
                                                                                                                                                                                               AAR50191;
                                                                                                                                        RESULT 13
                                                                                                                                                     AAR50191
                                                                                                                                                                                               ठे
                                                                                              d
```

Length 127;

DB 2;

Score 55;

100.08;

Query Match

```
..
                                                                                                                                                                                                                                                                       Kappa; light chain; murine; mouse; monoclonal; antibody; C225; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; chimeric; L7'CL; leader sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the kappa light chain variable region of the chimeric monoclonal antibody (MAb) C225, with the modified leader sequence from the kappa light chain of L7.CL MAb. C225 is specific for the human epidermal growth factor (EGF) receptor. C225, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage special tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 55; DB 2; Length 127; 100.0%; Pred. No. 0.0039; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goldstein NI, Giorgio NA, Jones ST, Saldanha JW;
                                                                                                                                                                                                                                           Kappa light chain variable region of C225 antibody.
                                                                                                                                       AAW08941 standard; protein; 127 AA.
100.08; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RASQSIGTNIH 11
                                                       1 RASOSIGINIH 11
                                                                                44 RASQSIGTNIH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RASOSIGINIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44
                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1:
AAW08941
```

us-09-635-974a-8.rag

```
Kappa, light chain, murine; mouse; monoclonal; antibody; M225; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the kappa light chain variable region of the murine monoclonal antibody (MAb) M225, which is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or displatin, or a signal transduction, ras or cell cycle inhibitor. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                     Kappa light chain variable region of M225 antibody.
                                                                                                                                                                                                                                                                                                                                                                                   Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                   Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example IV; Fig 13; 112pp; English.
                                                                                                                                                                                                                                                                                                                                       (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                 96WO-US009847.
                                                                                                                                                                                                                                                                                             95US-00482982.
                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-051897/05.
N-PSDB; AAT49338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 127 AA;
                                                                                                                                                                                                                                                                                          07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                      WO9640210-A1.
                                                                                                                                                                                                                                                               07-JUN-1996;
                                          27-AUG-2003
18-SEP-1997
                                                                                                                                                                                                                                   19-DEC-1996,
               AAW08941;
                                                                                                                                                                           Mus sp.
```

ö

0; Gaps

100.0%; Score 55; DB 2; Length 127; 100.0%; Pred. No. 0.0039; ative 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 11; Conservative

දු පු

Search completed: October 6, 2004, 16:29:46 Job time : 56.5789 secs

```
6, 2004, 16:34:15; Search time 37.3684 Seconds (without alignments) 51.669 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*

1: \cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: \cgn2_6/prodata/2/pubpaa/PCT_MEM_PUB_pep:*
3: \cgn2_6/prodata/2/pubpaa/NCT_MEM_PUB_pep:*
4: \cgn2_6/prodata/2/pubpaa/USO6_NEM_PUB_pep:*
5: \cgn2_6/prodata/2/pubpaa/USO6_NEM_PUB_pep:*
6: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PUB_pep:*
7: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PUB_pep:*
7: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PUB_pep:*
8: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PUB_pep:*
9: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PEP:*
11: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PEP:*
11: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PEP:*
13: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PEP:*
14: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PEP:*
15: \cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: \cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: \cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: \cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: \cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PUB_pep:*
17: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PUB_pep:*
18: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PUB_pep:*
18: \cgn2_6/prodata/2/pubpaa/USO8_NEM_PUB_pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1351062 seqs, 321799191 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                             US-09-635-974A-10
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seg length: 0
Maximum DB seg length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                             1 ASESIS 6
                                                                                                                                                                                                                  October
                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                              Run on:
```

|   |                          |                  |                   | Appl             | Appl             | App,              | App,              | 30831, A            | 046,                 | Appli             | 18, Appl         | 773,                 | Appl              | Appl             | Appl             | App               |
|---|--------------------------|------------------|-------------------|------------------|------------------|-------------------|-------------------|---------------------|----------------------|-------------------|------------------|----------------------|-------------------|------------------|------------------|-------------------|
|   |                          | 34,              | 10,               | 30,              | 40,              | 101               | 101               |                     |                      | 3,                | 18,              | 229.                 | 5, 7              | 28,              | 38,              | 129               |
|   | Description              | Sequence         | Sequence          |                  | Sequence         | Sequence          | Sequence          | Sequence            | Sequence             | Sequence          | Sequence         | Sequence 229773      | Sequence 25, Appl | Sequence         | Sequence 38,     | Segmence          |
|   | QI                       | US-09-798-689-34 | US-09-996-954B-10 | US-10-239-656-30 | US-10-239-656-40 | US-10-374-600-101 | US-10-374-531-101 | US-10-029-386-30831 | US-10-424-599-191046 | 5 US-10-379-151-3 | US-10-379-151-18 | US-10-424-599-229773 | US-09-991-470-25  | US-10-239-656-28 | US-10-239-656-38 | US-10-453-698-129 |
|   | - 1                      | 10               | 70                | 12               | 12               | 12                | 15                | 14                  | 12                   | 16                | 16               | 12                   | 6                 | 12               | 12               | 12                |
|   | Query<br>Match Length DB | 9                | φ                 | 7                | 7                | 7                 | 7                 | 19                  | 46                   | 19                | 61               | 88                   | 107               | 107              | 107              | 107               |
| æ | Query                    | 100.0            | 100.0             | 100.0            | 100.0            | 100.0             | 100.0             | 100.0               | 100.0                | 100.0             | 100.0            | 100.0                | 100.0             | 100.0            | 100.0            | 100.0             |
|   | Score                    | 25               | 25                | 25               | 25               | 25                | 25                | 25                  | 25                   | 25                | 25               | 25                   | 25                | 25               | 25               | 25                |
|   | Result<br>No.            | -                | 7                 | m                | 4                | Ŋ                 | 9                 | 7                   | 80                   | σ                 | 10               | 11                   | 12                | 13               | 14               | 15                |

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Sequence 45496, A Sequence 27, Appl Sequence 5606, Appl Sequence 1543, Ap Sequence 8, Appli            |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------|
| 10-374-600-113<br>10-374-600-113<br>10-374-600-114<br>10-374-531-113<br>10-374-531-114<br>10-374-600-22<br>10-374-600-23<br>10-374-600-23<br>10-374-600-23<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600-13<br>10-374-600- | US-10-767-701-45496<br>US-09-991-470-27<br>US-10-106-698-5606<br>US-09-764-864-1543<br>US-10-023-634-8 |
| 2 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                        |
| 1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>100                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 243<br>345<br>311<br>348                                                                               |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 000000                                                                                                 |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                        |
| 1111100000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ተ 4 4 4 4<br>4 4 4 4 4 6<br>13 6 4 6 6                                                                 |

## ALIGNMENTS

WESUNIT INCRANTION: US/09798689

# Sequence 34, Application US/09798689

# Publication No. US2003103973A1

# GENERAL INFORMATION: Detricia

# APPLICATION Rockwell, Patricia

# APPLICANT: Rockwell, Patricia

# APPLICANT: Goldstein, Neil I.

# TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF. Antagonists

# TITLE OF INVENTION: Combined With Radiation and Chemocherapy

# TITLE OF INVENTION: Combined With Radiation and Chemocherapy

# TITLE OF INVENTION: Combined With Radiation and Chemocherapy

# TITLE OF INVENTION: UNDER: US/09/798,689

# PRIOR FILING DATE: 1099-09-02

# PRIOR FILING DATE: 1999-09-03

# PRIOR FILING DATE: 1999-09-03

# PRIOR FILING DATE: 1995-06-03

# PRIOR FILING DATE: 1995-06-03

# PRIOR FILING DATE: 1994-02-10

# PRIO

1 ASESIS 6

ò

```
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
|||||||
2 ASESIS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ASESIS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-10-374-600-101
                                                                                        RESULT 4
US-10-239-656-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-23-03-30

Sequence 30, Application US/10239656

Publication No. US20040038339A1

GENERAL INFORMATION:
APPLICANT: KUFER, BETER
APPLICANT: LUTHERBUSE, RALF
APPLICANT: LUTHERBUSE, RALF
APPLICANT: MAYER, MONIKA
APPLICANT: HORMATION:
TITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
ITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
ITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
ITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
CURRENT APPLICATION NUMBER: US/10/239,656
CURRENT APPLICATION NUMBER: US/10/30-03-06
PRIOR FILING DATE: 2001-03-26
PRIOR PELING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: EP 00106467.4

PRIOR APPLICATION NUMBER: EP 00106467.4

PRIOR APPLICATION NUMBER: DATE 2001-03-24

PRIOR APPLICATION NUMBER: DATE 2001-03-24

PRIOR APPLICATION NUMBER: DATE 2001-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D OTHER INFORMATION: hybridoma 8G7C10 variable light chain CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                   Sequence 10, Application US/0996954B
Publication No. US20030157104A1
GENERAL INFORMATION:
TITLE OF INVENTION: Treatment of Refractory Human Tumors
TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
TITLE OF INVENTION: With Epidermal Growth Factor Receptor Antagonists
TITLE OF INVENTION: WITHER: US/09/996,954B
CURRENT APPLICATION NUMBER: US/09/996,954B
PRIOR PELING DATE: 04-24-2001
PRIOR APPLICATION NUMBER: 09/314,028
PRIOR APPLICATION NUMBER: 09/312,284
PRIOR PELING DATE: 05-14-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 25; DB 12; Length 7 Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 10;
100.0%; Pred. No. 1.2e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT , ORGANISM: Homo sapiens-Rodent Chimera US-09-996-9548-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ASESIS 6
                                                                  US-09-996-954B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-10-239-656-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-239-656-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
```

```
APPLICANT: KUFER, PETER
APPLICANT: KUFER, PETER
APPLICANT: KUFTERUSE, REALF
APPLICANT: LUTTERUSE, RALF
APPLICANT: BORSCHERT, KATRIN
APPLICANT: MAYER, WONIKA
APPLICANT: MOUNTIPUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
TITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
FILE REFERENCE: 029976/0106
CURRENT APPLICATION NUMBER: US/10/239,656
CURRENT APPLICATION NUMBER: EP 00106467.4
PRIOR PILING DATE: 2001-03-24
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PATENTING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PATENTING NOS: 92
SOFTWARE: PATENTING NO 40
TEMPLY APPLICATION VANCE: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D; OTHER INFORMATION: hybridoma 6E5A7 variable light chain CDR2
US-10-239-656-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 101, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 25; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/10239656
Publication No. US20040038339A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & J
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
1 ASESIS 6
```

```
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 ASESIS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ASESIS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-424-599-191046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-374-531-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5-10-3, -3-31-1. Application US/10374531
Sequence 101, Application US/20040006212A1
Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INFIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 12; Length 7; 100.0%; Pred. No. 1.2e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10004

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                              ALOCKMET FORM INCOMMINENT INCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION NUMBER: US/09/37,065C
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT: INFORMATION:
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING:DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon STREET: One Broadway
CITY: New York STATE: New York COUNTRY: US
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASESIS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-10-374-531-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

```
US-10-029-386-30831

US-10-029-386-30831

Sequence 30831, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

COURRENT APPLICATION UNDHER: US/10/029,386

CURRENT APPLICATION UNDHER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SEQ ID NOS: 34288

LENGTH: 19

SEQ ID NO 30831

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 191046, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: And Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 14; Length 19; 100.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEATURE:
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 15; 100.0%; Pred. No. 1.2e+06;
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 425-7200
TELEFRAX: (212) 425-7200
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acids
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECILE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 6; Conservative
```

```
Squence 229773, Application US/10424599
Squence 229773, Application US/10424599
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/09991470

Sequence 25, Application US/09991470

Sequence 25, Application US/09991470

Sequence 25, Application US/09991470

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION WUMBER: US/09/991,470

CURRENT FILING DATE: 2001-11-20

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-16

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FESTESEQ for Windows Version 4.0

SEQ ID NO 25

LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 25; DB 9; Length 107; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                  100.0%; Score 25; DB 16; Length 61; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_49509C.1.pep
US-10-424-599-229773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 12;
100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0;
                                                                      FEATURE:
; OTHER INFORMATION: Cloned Antibody CDR Sequences
US-10-379-151-18
                         TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                             Query Match
Best Local Similarity 100...
Feet Gooservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: human/murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 ASESIS 31
                                                                                                                                                                                                                                                                    1 ASESIS 6
                                                                                                                                                                                                                                                                                                             2 ASESIS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                US-10-424-599-229773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 229773
LENGTH: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-991-470-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-991-470-25
       LENGTH: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/10379151
Fublication No. US20040175692A1
GENERAL INFORMATION:
APPLICANT: Alexion Pharmaceuticals, Inc.
APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdish, Katherine S.
APPLICANT: McWhitter, John
TITLE OF INVENTION: CHRONIC LYMPHOCYTIC LEUKEMIA CELL LINE
TILE REFERENCE: 60 CIP (1087-43 CIP)
CURRENT APPLICATION NUMBER: US/10/379,151
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: PCT/US01/47931
PRIOR APPLICATION NUMBER: PCT/US01/47931
PRIOR APPLICATION NUMBER: US 60/254,113
PRIOR PILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10379151
Sequence 3, Application US/10379151
Publication No US20040175692A1
GENERAL INCORMATION:
APPLICANT: Alexion Pharmaceuticals, Inc.
APPLICANT: Bowdish, Katherine S.
APPLICANT: Mowhirter, John
TILLE OF INVENTION: CHRONIC LYMPHOCYTIC LEUKEMIA CELL LINE
FILE REFERENCE: 60 CIP (1087-43 CIP)
CURRENT APPLICATION NUMBER: US/10/379,151
CURRENT PILING DATE: 2003-06-24
FRIOR APPLICATION NUMBER: US 60/254,113
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-08
NUMBER OF SEQ ID NOS: 26
SOFFWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 100.0%; Score 25; DB 16; Length 61; Similarity 100.0%; Pred. No. 1e+02; 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                Length 46;
                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                             ; CTHER INFORMATION: Clone ID: PAT_MRT3847_14533C.1.pep
US-10-424-599-191046
                                                                                                                                                                                                                                           Query Match
100.0%; Score 25; DB 12;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Cloned Antibody CDR Sequences
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191046
LENGTH: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: artificial sequence
                                                                                                  TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         36 ASESIS 41
                                                                                                                                                                                                                                                                                                                                           1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                         음
```

```
LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                         엄
                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KUFER, PETER
APPLICANT: KUFER, PETER
APPLICANT: KUFER, GERT
APPLICANT: LITERBUSE, RALF
APPLICANT: LITERBUSE, RALF
APPLICANT: MISCHEL, ROMAN
APPLICANT: MAYER, MONIKA
APPLICANT: MAYER, MONIKA
APPLICANT: MONESTER, ROBERT
TITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
TITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
TITLE OF INVENTION: UNMBRR: US/10/239, 656
CURRENT APPLICATION NUMBER: US/10/239, 656
CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: PCT/EP01/03414
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 107
THENDER OF SET OF SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/10239656

Publication No. US2004003839A1

GENERAL INFORMATION:
APPLICANT: KUPER, PETER
APPLICANT: BUTTERBUSE, RALF
APPLICANT: MAYER, WONIKA
APPLICANT: MAYER, WONIKA
APPLICANT: MAYER, WONIKA
APPLICANT: MAYER, WONIKA
APPLICANT: MONIKA
APPLICANT: MONIKA
APPLICANT: MOSTER, ROBERT
TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPLEX
TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPLEX
CURRENT APPLICATION NUMBER: US/10/239,656
CURRENT APPLICATION NUMBER: DC10-03-06
PRIOR FILING DATE: 2003-03-06
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 92
SOFTWARE PATENTIN VEY: 2.1
SEQ ID NO 38
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D; OTHER INFORMATION: hybridoma 8G7C10 variable light chain US-10-239-656-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 25; DB 12; Length 107; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                        Sequence 28, Application US/10239656
Publication No. US20040038339A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
|||||||
51 ASESIS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 ASESIS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ASESIS 6
                                              쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D; OTHER INFORMATION: hybridoma 6E5A7 variable light chain US-10-239-656-38
                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                     Gaps
                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                      Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 12; Length 107; 100.0%; Pred. No. 1.9e+02;
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                    Query Match
100.0%; Score 25; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rother, Russell
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
SEQ ID NO 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: October 6, 2004, 17:09:05 Job time: 37.3684 secs
                                                                                                                                                                                                                                                                                                                                ; Sequence 129, Application US/10453698; Publication No. US20040038308A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 6, Conservative
                                                                                                                                                                                                                  51 ASESIS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 ASESIS 56
                                                                                                                                                                             1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                    RESULT 15
US-10-453-698-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-453-698-129
```

This Page Blank (uspto)

Sequence:

Run on:

Database

Result

```
Sequence 28, Appl
Sequence 90, Appl
Sequence 3, Appli
Sequence 1, Appli
Sequence 1776, Ap
Patent No. 526870, Ap
Sequence 2, Appli
Sequence 19, Appl
Sequence 19, Appl
Sequence 110, Appl
Sequence 11, Appli
Sequence 13, Appli
Sequence 63, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: FALLS CHOKEN
STATE: VA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/232,0818
US-09-195-868-28
US-08-476-3494-90
US-08-476-3494-90
US-08-589-939-3
US-09-244-369B-1
US-09-540-236-3776
US-09-541-81B-19
US-09-541-81B-19
US-09-548-436-19
US-09-339-922A-108
US-09-339-922A-108
US-09-339-922A-108
US-09-339-922A-108
US-09-339-922A-108
US-09-339-922A-108
US-09-339-922A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIRCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 2;
illarity 100.0%; Pred. No. 3e+05;
Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: WIJDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIR
STREET: PO BOX 747
CORREST: AND CONTROL CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CONTROL
CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INPORMATION:
NAME: SYENSSON, LECNARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPAK: (703) 205-8050
TELEPAK: (703) 205-8050
TELEPAK: (703) 205-8050
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: A mino acids
TYPE: amino acids
STRANEDNESS: not relevant
      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ASESIS 6
      1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-08-232-081B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-232-081B-5
         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 54, Appl
Sequence 54, Appl
Sequence 4, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Appl
Sequence 4, Appli
Sequence 8, Appli
Sequence 8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10, Appl
6, Appli
8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appl
                                                                                                                                                                                                   October 6, 2004, 16:24:54 ; Search time 10.6316 Seconds (without alignments) 29:135 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Ap Sequence 4, Ap Sequence 40, Ap Sequence 4, Ap Sequence 4, Ap Sequence 6, Ap Sequence 10, Ap Sequence 8, Ap Sequence 10, Ap Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, A
Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lssued_Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-232-081B-5
US-08-476-176B-54
US-08-485-246A-54
US-09-195-868-23
US-09-296-595-4
US-09-296-595-4
US-08-232-081B-9
US-08-232-081B-9
US-08-476-176B-4
US-08-476-176B-6
US-08-476-176B-6
US-08-476-176B-6
US-08-476-176B-6
US-08-485-246A-9
US-08-127-721A-10
US-08-127-721A-6
US-08-127-721A-6
US-08-127-721A-10
US-08-127-721A-6
US-08-127-721A-10
US-08-127-721A-10
US-08-127-721A-10
US-08-127-721A-10
US-08-127-721A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-800-198-8
US-09-296-595-8
US-09-510-322A-10
US-09-195-868-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                          US-09-635-974A-10
25
1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
```

ö

Gaps

. 0

```
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-127-721A-54

J Sequence 54, Application US/08127721A

Sequence 54, Application US/08127721A

Patent No. 6066718

GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6066718artis Patent and Trademark Department
STREET: 59 Route 10
CITY: East Hanover
                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958708artis Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 2; Length 7; 100.0%; Pred. No. 3e+05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            ADDRESSE: No. 5958708artis Patent Department STREET: 59 Route 10 CITY: Bast Houver STATE: New Jersey COUNTRY: USA ZIP: USA ZIP: O'7936-1080 COMPUTER READABLE FORM: WEDIUM TYRE: TIOPPY disk COMPUTER: ISW PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: 08 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/POCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPRAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHRACATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                         ; Sequence 54, Application US/08476176B
; Patent No. 5958708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-476-176B-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ASESIS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
```

```
COUNTRY: 1084

ZETP: 07395-1080

ZETP: 07395-1080

COMPUTER REPAIRED FORM: 10.64

FILLING DATE: 24

FRIEND DATE: 24

FRIEND DATE: 10.65

FRIEND FORM: 1
```

ö

28 ASESIS 33

셤

```
Sequence 4, Application US/08800198
Patent No. 5542602
GENERAL INFORMATION
APPLICANT: WELS, WINPRIED S.
APPLICANT: SCHNIDT, MATHASA
APPLICANT: SCHNIDT, MATHASA
APPLICANT: SCHNIDT, WATHASA
APPLICANT: SCHNIDT, WATHASA
APPLICANT: SCHNIDT, WATHASA
APPLICANT: SCHNIDT, BROWTH FACTOR RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,198
FILING DATE: 13-FEB-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/POCKET NUMBER: SCH 1576
TELEPONE: 103-243-6333
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C. STREET: 2200 CLARENDON BLVD. SUITE 1400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC compa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 703-243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 ASESIS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FRAGMENT TYPE:
US-08-800-198-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 25; DB 3; Length 99; Best Local Similarity 100.0%; Pred. No. 23; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 3; Length 7; 100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: KAVANAUGH MD, MICHAEL
APPLICANT: KAVANAUGH MD, MICHAEL
APPLICANT: WILLIAMS MDPHD, LEWIS T.
TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE
TITLE OF INVENTION: 5-PHOSPHATASES (SIPs)
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 HORION STREET
STATE: CHIRON CORPORATION
CITY: EMERYVILLE
STATE: CHIRON CORPORATION
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94608

ZIP: 94608

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,868
                                 4-19276/A/P2/CIP
                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
APPLICATION:
APPLICATION NUMBER: US/09/195,868
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FIRESTONE, LEIGH H.
REFERENCE/DOCKET NUMBER: 182,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-623-2707
TELEPHONE: 510-65-3542
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/09195868 Patent No. 6090621
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                           ) MOLECULE TYPE: protein US-08-485-246A-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASESIS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA
                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-195-868-23
                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
ö
                                                   Gaps
                                                   .;
0
; Score 25; DB 2; Length 106;
; Pred. No. 25;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                        Sequence 4, Application US/09296595A;
Sequence 4, Application US/09296595A;
Patent No. 6129915;
GENERAL INFORMATION:
SAPPLICANT: WIFFIED S.
APPLICANT: SCHNIDT, MATHIAS;
APPLICANT: SCHNIDTER, DOUGLAS;
TILLE REFERENCE: SCH-1276 D1
CURRENT APPLICATION NUMBER: US/09/296,595A;
CURRENT PILING DATE: 1999-04-23;
EARLIER REPLING DATE: 1997-02-13;
NUMBER OF SEQ ID NOS: 18
100.0%;
```

```
NAKATANI, TOMOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                      STATE: Vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                      ö
                                                                                                                                                                      ö
                                                                                                                              100.0%; Score 25; DB 3; Length 106; 100.0%; Pred. No. 25; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 25; DB 2; Length 107; Best Local Similarity 100.0%; Pred. No. 25; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: NAKATHI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: MJUDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
ITILE OF INVENTION: HURANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/232,081B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-3484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08232081B Patent No. 5886152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: SYENSON, LEONARD R
REGISTRATION NUMBER: 30,330
REPRENCE/DOCKET NUMBER: 20-34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 107 amino acids
TYPE: amino acid
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 106
                                                                                                                  Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 ASESIS 56
                                                                        , ORGANISM: Murine sp
US-09-296-595-4
                                                                                                                                                                                                                                                  51 ASESIS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASESIS 6
                                                                                                                                                                                                            1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-232-081B-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-232-081B-9
                                                                                                                                                                                                                                                                                                          RESULT 8
US-08-232-081B-9
                                                            TYPE: PRT
                                                                                                                                                                                                                                                  d
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hardman, No. 5958708man
APPLICANT: Hardman, No. 5958708man
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
STREET: 59 Route 10
STREET: New Jersey
COUNTRY: USA
ZIP: 07936-1008
CONDITY: BEAL Hanover
STATE: New Jersey
COUNTRY: USA
MEDIUM IYPE: Floppy disk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 2; Length 107; 100.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
APPLICANT: GOMI, HIDEYUKI
APPLICANT: MJDENES, JOHN
APPLICANT: NJOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
NUMBER OF SEQUENCES: 42
NUMBER OF SEQUENCES: 42
NUMBER OF SEQUENCES: 42
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22640-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/232,081B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08476176B Patent No. 5958708
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFRENCE/DOCKET NUMBER: 20-3.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 107 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-232-081B-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 ASESIS 56
```

```
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 107 amino acids
amino acid
Query Match
Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-485-246A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 ASESIS 56
                                                                                                                                                                 1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                  US-08-485-246A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-476-176B-6
                                                                                                                                                                     ð
                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Adladna, Jose
TITLE OF INVENTION:
TITLE OF INVENTION: Immunoglobulin isotype
TITLE OF INVENTION: Immunoglobulin isotype
TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Now. 6066718artis Patent and Trademark Department
STREET: New Jersey
COUNTRY: USA
ZIP: New Jersey
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DSKNS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION NUMBER: US 07/952,802
FILING DATE: 28-SEPTEMBER-1993
CLASSIFICATION NUMBER: US 07/952,802
FILING DATE: 28-SEPTEMBER-1993
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 33,200
REFERENCE/COCKET NUMBER: 33,200
RESERVENCE/COCKET NUMBER: 33,200
RESERVENCE/CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 2; Length 107; 100.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                 APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: 08/07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEFAX: (908) 277-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08127721A Patent No. 6066718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 107 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-476-176B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
Matches	S. Milarity	100.04; Score 25; DB 3; Length 107;			
Matches	S. Conservative	O; Mismatches	O; Indels	O; Gaps	O;
Matches	S. Conservative	O; Mismatches	O; Indels	O; Gaps	O;
Matches	S. Conservative	O; Mismatches	O; Indels	O; Gaps	O;
Matches	S. Milarity	Oscillation	O		
```

```
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08476176B
Patent No. 5958708
GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 25; DB 2; Length 127; Best Local Similarity 100.0%; Pred. No. 31; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                   ADDRESSER No. 5958708artis Patent Department
STRET: 59 Route 10
CITY: East Hanover
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING REASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 55 CORRESPONDENCES SECONDENCE ADDRESSE: ADDRESSE: No. 5958708artis Patent Department STREET: 59 Route 10 CITY: East Hanover STATE: New Jersey COUNTY: USA COUNTRY: USA MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPUTER: OF COMPUTER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLIASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 25-SEPTEMBER-1993
PTLING DATE: 25-SEPTEMBER-1992
PTLING DATE: 15-SEPTEMBER-1992
ATOMORE: No. 5958708aK, Henry P.
REGISTRATION NUMBER: 33,200
REFENCE/DOCKET NUMBER: 34,200
REFENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-5110
TELEPHONE: (908) 277-510
TELEPHONE: (908) 277-510
TELEPHONE: (908) 277-510
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 127 anino acida TOPOLOGY: 1-27 anino acida Olemnia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-476-176B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 ASESIS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-476-176B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08476176B
Patent No. 5958708
GADERAL INFORMATION:
GADELICANT: Hardman, No. 5958708man
APPLICANT: Kalbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 2; Length 127; 100.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
PRING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: 05 07/952,802
FILING DATE: 125-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708 AK, Henry P.
REGISTRATION NUMBER: 33,200
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELEPHONE: (908) 277-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 22-SEPTEMBER-1993
FILING DATE: 25-SEPTEMBER-1992
FILING DATE: 25-SEPTEMBER-1992
ATOCNEV, AGENT INCORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REGISTRATION NUMBER: 34-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                      TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 127 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity luv.
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               East Hanover: New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 ASESIS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-476-176B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-476-176B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: N
```

This Page Blank (uspro)

Wede to

|                                       | Copyright (c) 1993 - 2004 Compugen Ltd.                                                                     |
|---------------------------------------|-------------------------------------------------------------------------------------------------------------|
| OM protein - pr                       | OM protein - protein search, using sw model                                                                 |
| Run on:                               | October 6, 2004, 16:20:48; Search time 30.3158 Seconds (without alignments) 55.921 Million cell updates/sec |
| Title:<br>Perfect score:<br>Sequence: | US-09-635-974A-10<br>25<br>1 ASESIS 6                                                                       |

Total number of hits satisfying chosen parameters: 1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A Geneseq 29Jan04:\* 1: geneseqp1980s:\* geneseqp1980s:\* geneseqp1990s:\* Database

geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | Aay59315 Light cha | ø        | Aau77788 Mouse lig | Ą        | Aay26991 CDR2 doma | 4        | N        | 09       | Abb79661 Chronic 1 | Aag18882 Zea mays | 33       | 5 Anti   | Aaw71241 Light cha | Aar32129 Anti-IL2R | Aar37610 B-B10 MAb | N        | _        | Aaw08949 Kappa lig | Aaw08948 Kappa lig | Aay26979 Light cha | 4        | 2        | 0 Anti-N | Aao16010 Mouse int | Abb80270 Vitaxin l |
|-----------|----------------|--------------------|----------|--------------------|----------|--------------------|----------|----------|----------|--------------------|-------------------|----------|----------|--------------------|--------------------|--------------------|----------|----------|--------------------|--------------------|--------------------|----------|----------|----------|--------------------|--------------------|
| SUMMARIES | ID             | AAY59315           | AAB37956 | AAU77788           | AAR37603 | AAY26991           | AAU72844 | AAU72852 | ABB79660 | ABB79661           | AAG18882          | AAG18881 | AAW26795 | AAW71241           | AAR32129           | AAR37610           | AAR37612 | AAR50190 | AAW08949           | AAW08948           | AAY26979           | AAY70604 | AAU72842 | AAU72850 | AA016010           | ABB80270           |
|           | DB             | i<br>m             | 4        | 'n                 | 7        | ~                  | w        | 'n       | Ŋ        | Ŋ                  | ო                 | m        | ~        | ~                  | ~                  | ~                  | ~        | ~        | ~                  | ~                  | ~                  | m        | ហ        | w        | Q                  | 7                  |
|           | Length         | 9                  | φ        | 9                  | 7        | 7                  | 7        | 7        | 61       | 61                 | 82                | 8        | 104      | 106                | 107                | 107                | 107      | 107      | 107                | 107                | 107                | 107      | 101      | 107      | 107                | 107                |
| <b></b>   | Query<br>Match | 100.0              | 100.0    | 100.0              | 100.0    | 100.0              | 100.0    | 100.0    | 100.0    | 100.0              | 100.0             | 100.0    | 100.0    | 100.0              | 100.0              | 100.0              | 100.0    | 100.0    | 100.0              | 100.0              | 100.0              | 100.0    | 100.0    | 100.0    |                    | 100.0              |
|           | Score          | 25                 | . 52     | 25                 | 25       | 25                 | 25       |          |          | . 25               |                   | 25       | 25       | 25                 | 25                 | 25                 | 25       | 25       | 25                 | 25                 | 25                 | 25       | 25       | 25       | 25                 |                    |
|           | Result<br>No.  |                    | 01       | ٣                  | 4        | Ŋ                  | 9        | 7        | 80       | 6                  | 10                | 11       | 12       | 13                 | 14                 | 15                 | 16       | 17       | 18                 | 19                 | 20                 | 21       | 22       | 23       | 24                 | 25                 |

| A V V V V V V V V V V V V V V V V V V V                                                                                                                                                                                | Abp96765 TSH recep<br>Adc79230 OC125-3.1<br>Adw26625 Signallin<br>Aar34511 Fv(TU25). |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|
| ADD13784<br>AAP90479<br>AAR50197<br>AAR501191<br>AAR501191<br>AAW08946<br>AAW08946<br>AAW08946<br>AAW08946<br>AAW26980<br>AAY26980<br>AAY26980<br>AAY26980<br>AAY26980<br>AAY26980<br>AAY36987<br>ABP96756<br>ABP96756 | ABP96765<br>ADC79230<br>AAW26625<br>AAR34511                                         |
| 11111111111111111111111111111111111111                                                                                                                                                                                 |                                                                                      |
|                                                                                                                                                                                                                        | 0000                                                                                 |
|                                                                                                                                                                                                                        | 0000                                                                                 |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                  | 0 0 0 0<br>0 0 0 0                                                                   |
|                                                                                                                                                                                                                        | 4 4 4 4<br>2 6 4 7                                                                   |

## ALIGNMENTS

Hypervariable region, complementarity determining region, CDR, tumour, single chain antibody, growth inhibitor; human, tumourigenesis, therapy, protein receptor tyrosine kinase, light chain. Robert F, Buchsbaum DJ; Light chain hypervariable region, CDR2 AAY59315 standard; peptide; 6 AA. 98US-00079612. 98US-0085613P. 98US-00206138. 99WO-US010741 (IMCL-) IMCLONE SYSTEMS INC. (UABR-) UAB RES FOUND. (first entry) Waksal HW, Saleh MN, 15-MAY-1998; 15-MAY-1998; 07-DEC-1998; WO9960023-A1. 14-MAY-1999; 07-MAR-2000 25-NOV-1999. AAY59315; Mus sp. 

WPI; 2000-062440/05. N-PSDB; AAZ48629.

Treatment of human tumors, using a combination of radiation and a non-radiolabeled protein receptor tyrosine kinase inhibitor.

Disclosure; Page 15; 31pp; English.

This sequence is the hypervariable region CDR2 (complementarity determining region 2) of the light chain of a single chain antibody deterived from the murine antibody 225. The invention relates to a method for inhibiting the growth of tumours in human patients by treating with an effective amount of a combination of radiation and a non-radiolabelled protein receptor tyrosine kinase (RRTK) inhibitor, the overexpression of which can lead to tumourigenesis. The method can be used in the treatment of tumours of e.g. breast, lung, colon, kidney, bladder, head and neck, ovary, prostate or brain. The administration of a suitable antibody to

AAU77788 standard; peptide; 6 AA.

RESULT

ASESIS 6

(first entry)

05-JUN-2002

AAU77788;

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a method for inhibiting the growth of factactory tumours that are stimulated by a ligand of epidermal growth factor receptor (EGFR) in human patients. The method involves treating the patient with a combination of EGFR/human EGF-1 (HERI) antagonist, optionally with a chemotherapeutic agent or radiation. The antagonist can be for example a chimeric anti-EGFR monoclonal antibody, C25. The EGFR/HERI antagonist is useful for inhibiting the growth of refractory tumours such as tumours of breast, heart, lung, small intestine, colon, skin, bone, bone marrow, hlood, thymus, uterus, testicles, cervix and liver, preferably squamous cell carcinomas. The present sequence liver, preferably squamous cell carcinomas. The present sequence region 2 amino acid sequence of the chimeric anti-EGFR monoclonal antibody C225 which is used in an example illustrating the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Epidermal growth factor receptor/human epidermal growth factor receptor-1 antagonist for inhibiting the growth of refractory tumors.
                                                                                                                                                                                                                                                                                                                                                                                          Refractory tumour growth inhibition; epidermal growth factor receptor; EGFR antagonist; cancer; squamous cell carcinoma; anti-EGFR antibody; complementarity determining region; CDR.
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                         Anti-EGFR monoclonal antibody L chain V region CDR2 peptide sequence.
                                                                                                  ;
0
the patient makes the tumour more susceptible to radiotherapy
                                                               Similarity 100.0%; Score 25; DB 3; Length 6; Similarity 100.0%; Pred. No. 1.4e+06; 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 14; 31pp; English.
                                                                                                                                                                                                                                                     AAB37956 standard; protein; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00312284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000; 2000WO-US011756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-016160/02.
                                                             Query Match
Best Local Similarity
                                                                                                                                    1 ASESIS 6
                                                                                                                                                                   ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC83239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200069459-A1.
                                Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAY-1999;
13-AUG-1999;
                                                                                                                                                                                                                                                                                                                          12-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waksal HW;
                                                                                                                                                                                                                                                                                        AAB37956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
                                                                                                  Matches
                                                                                                                                                                                                                    요
```

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel method for treating a mammal with hyperproliferative disease stimulated by a ligand of a member of the epidermal growth factor (EGP) family of receptors. The method involves administering an antibody or a defective receptor that is an antagonist of a member of the EGF receptor family, or a combination of the rantagonist and photocherapy, chemotherapeutic agent or radiation therapy. The antibody used in the method of the invention acts as an epidermal prosphorylation. The method of the invention is useful for treating a mammal with hyperpoliferative disease such as psoriasis, actinic structured by a ligand of a member of the EGF family of receptor. This sequence represents the murine anti-EGF 25s antibody light chain (LH) hypervariable region (CDR2) used as an inhibitor of EGFR in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating a mammal with hyperproliferative disease especially psoriasis, stimulated by ligand of member of epidermal growth factor family of receptors, by administering antagonist of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                              Mouse; light chain; antibody; hyperproliferative disease; epidermal growth factor; EGF; psoriasis; actinic keratosis; seborrheic keratosis; warts; keloid scars; eczema; 255 antibody; hypervariable region; CDR2; EGFR inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                 Mouse light chain hypervariable region (CDR2) of 225 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 5; L
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 12; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR37603 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                          09-AUG-2001; 2001WO-US041647.
                                                                                                                                                                                                                                                                                                                                           09-AUG-2000; 2000US-00635974.
                                                                                                                                                                                                                                                                                                                                                                          (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-257423/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABK11444.
                                                                                                                                                                                                                                       WO200211677-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the invention
                                                                                                                                                                                                                                                                          14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                            reufel T;
                                                                                                                                                                                                        Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
AAR37603
ID AAR3
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

ö

Gaps

;

100.0%; Score 25; DB 4; Length 6; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels

Conservative

1 ASESIS

Local Similarity

Best Loc Matches

Query Match

```
The invention relates to a method of determining IgE levels in a body fluid sample, by contacting the sample with a reshaped human monoclonal antibody (RA) having a binding affinity about equal to that of the murine CDR-donor antibody TES-C21 produced by the cell line 11133. The antibodies are useful in the diagnosis, prophylaxis and treatment of allergy. This sequence represents the complementarity determining region (CDR) 2 from the light chain variable domain of a reshaped human antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, NKG2D, NKG2D receptor complex; cancer; infectious disease; tumour; autcimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; mysloma; Farcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7B7; 8G7C10; 6ESA7; 11B2D104,7; 6ESA74,11B2D104,7; 6ESA74,11B2D104,7; 6ESA74-7; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; BB10xP4-3; BB10xP4-3; BA14; p53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
    binding affinity; mouse; CDR; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 2; Length 7; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-NKG2D hybridoma 8G7C10 variable light chain CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       new method for determining IgE levels in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                            Saldanha J, Kolbinger F, Hardman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU72844 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Col 67; 19pp; English
                                                                                                                                                                                                                              95US-00476176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2001; 2001WO-EP003414.
                                                                                                                                                                                                                                                                                                                                       (NOVS ) NOVARTIS CORP.
(TANO-) TANOX BIOSYSTEMS INC.
                                                                                                                                                                                                                                                                         92US-00952802
93US-00127721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-570765/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ASESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200171005-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 AA;
                                                                                        Homo sapiens
                                                                                                                                                                                                                                07-JUN-1995;
                                                                                                                                                                                                                                                                         25-SEP-1992;
27-SEP-1993;
                                                                                                                                        US5958708-A.
                                                                                                                                                                                28-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001,
                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU72844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                               allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAR37599-604 represent the complementarity-
determining regions (CDRs) of a humanised antibody (Ab) which binds

CC specifically to human interleukin (II)-2 receptor (HIL2R). These CDRs

CC were derived from the murine anti-human IL-2 receptor monoclonal Ab (MAD)

CC HIL-2 to the IL-2 receptor on human T-cells. It also inhibits the human

CC IL-2 to the IL-2 receptor on human T-cells. It also inhibits the human

CC IL-2 to the IL-2 receptor on human T-cells. It also inhibits the human

CC IL-2 to the IL-2 receptor on human T-cells. It also inhibits the human

CC IL-2 to the IL-2 receptor on human T-cells. It also inhibits the human

CC IL-2 to the IL-2 receptor on human T-cells. It also inhibits the human

CC IL-2 to the IL-2 receptor on human T-cells. It also inhibits the human

CC IL-2 to the IL-2 receptor on human T-cells. It also also AAQ43226-32 and

AAQ43233-36). A human Ab with high levels of amino acid sequence homology

CC to the murine sequence cans selected and the framework to design

Several kinds of the humanised B-B10 V region (see also AAQ43244-45). The

DNA sequence coding this humanised B-B10 was synthesised and a plasmid

expressing humanised B-B10 was constructed. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised antibody comprising - CDR region of mouse MAB B-B10 specific for IL-2 receptor useful for treating carcinoma expressing IL-2 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosis, IgE; immunoglobulin; body fluid; human; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                        Complementarity-determining region; CDR; humanised; antibody; hILL2R; human; incerleukhn; IL-2; receptor; murine; anti-human; Ab; T-cell; monoclonal antibody; B-Bl0; mixed lymphocyte reaction; variable; V; region; PCR; framework; plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDR2 domain reshaped human antibody light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 2; Length 7; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noguchi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wijdenes J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY26991 standard; protein; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 43; 62pp; English.
                                                                                                           hIL2R Ab L chain V region CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUMU ) SUMITOMO PHARM CO LTD. (BIOT ) BIOTEST PHARMA GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     91JP-00323319.
                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INNO-) INNOTHERAPIE LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakatani T, Gomi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-197057/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                 WO9311238-A1
                                                                                                                                                                                                                                                                                                                                                                                                        03-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-1991;
                                                                                                                                                                                                                                                                         Mus musculus
                                           25-MAR-2003
13-OCT-1993
                                                                                                                                                                                                                                                                                                                                                            10-JUN-1993
AAR37603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY26991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY26991
ID AAY:
XX AAY:
XX DT 24-1
XX DE CDR
XX XX DIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
```

à 셤

ô

Gaps

;

Kischel R;

Borschert K,

```
The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group in the NG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated controlled in the properties and its associated polymolectide are used for the preparation of a pharmaceutical composition. The cancer may be a tumour of the head and neck, stomach, conditions. The cancer may be a tumour of the head and neck, stomach, cosophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larged are relative, breast, oversy, uterus, cervix, prostate, kidney, testis, thyroid, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protocoa or helminths. The autoimmune diseases include multiple clerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent autoimmune hepatitis. Squences AM172810-AM172875 represent the NKG2D receptor and the polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breast; uterns; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv sarcoma; lenkaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; ll82D10; 6H7B7; 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 8G5A7x4-7; P4-2; P4-3; P4-14; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-13; B4-14; p5-3 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
                                                                                                                                                                                 Multifunctional polypeptides comprising binding sites that specifically recognize extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h Similarity 100.0%; Score 25; DB 5; Length 7; Similarity 100.0%; Pred. No. 1.40+06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-NKG2D hybridoma 6E5A7 variable light chain CDR3.
                                                                                Lutterbuese R,
                                                                                                                                                                                                                                                                                        Example 3; Fig 16; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU72852 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2001; 2001WO-EP003414.
24-MAR-2000; 2000EP-00106467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                o,
                                                                                Riethmueller
Hofmeister R;
                                                                                                                                            WPI; 2002-055119/07
                                                                                                                                                                                                                                                  infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASESIS 7
                                         (KUFE/) KUFER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200171005-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2001
                                                                                Kufer P,
Mayer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU72852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

```
The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NK3Dz receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, cosphagus, colon, liver, intrahepatic bile ducts, pancreas, lung, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious disease, autoimmune diseases include multiple sclerosis, drave's disease, autoimenne diseases include multiple sclerosis, drave's disease, antwicklesing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent autoimmune hepatitis. Squances, ANUZSEO-ANUZSEO represent the NKG2D autoimmune hepatitis. Squances ANUZSEO-ANUZSEO represent the NKG2D creceptor and the polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "light chain complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "light chain complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "light chain complementarity determining region 3"
                                                                                                                                                      Multifunctional polypeptides comprising binding sites that specifically recognize extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                     Kischel R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chronic lymphocyte leukaemia specific scFv Elc CDR sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chronic lymphocytic leukaemia; CLL; scFv; antibody; rabbit; complementarity determining region; CDR; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                       Borschert K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 5; L
100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
                                                                       Lutterbuese R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                   Example 3; Fig 16; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB79660 standard; protein; 61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .11
/label= LC-CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12. .18
/label= LC-CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19. .28
/label= LC-CDR3
24-MAR-2000; 2000EP-00106467.
                                                                     Riethmueller G,
Hofmeister R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus.
                                                                                                                                                                                                                   infectious diseases.
                                                                                                                          WPI; 2002-055119/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ASESIS 7
                                     (KUFE/) KUFER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-OCT-2002
                                                                       Kufer P,
Mayer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB79660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB79660
   ò
```

ö

Gaps

. 0

Oryctolagus cuniculus.

```
The present sequence comprises a summary of the complementarity determining regions (CDRs) of the light chain and heavy chain of the arboric lymphocytic leukaemia (CLLs Specific rabbit serv antibody Elecantic Lymphocytic leukaemia (CLLs Specific rabbit serv antibody Elecantic Sequence. Rabbit scrv antibodies (see ABB79657-81) for B-CLL-specific sequence. Rabbit scrv antibodies (see ABB79657-81) for B-CLL-specific cell surface panning. The invention provides a CLL line, CLL-AAT, derived from a B-CLL primary line without immortalisation by Epstein-Barr virus. The cell line is used to generate antibodies useful in the diagnosis and/or treatment of CLL. Antibodies derived from recombinant libraries may be selected using CLL-AAT as bait to isolate antibodies on the basis of specificity. Single chain antibodies are of particular use as they remain stable in the cytoplasm and retain intracellular binding activity. The binding of the present scrv antibody to primary human cells and cell coll mines was determined by whole cell ELISA as follows: CLL (primary thumunes and CLL-AAT cell line) ++; normal, primary human B lymphocytes, +; non-fody human erythnolukaemia cell line RL -; Burkitt's lymphoma cell line Ramos, and human erythnolukaemia cell line TF-1, - A short linker separates the VL and VH regions of the scrv. The antigen recognised by this scrv was CD23, determined by immunoprecipitation and mass spectrometry
34. .48
/label= HC-CDR2
/lote= "heavy chain complementarity determining region 2"
49. .61
/label= HC-CDR3
/note= "heavy chain complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chronic lymphocytic leukemia cell line (designated CLL-AAT), useful for studying, diagnosing or treating chronic lymphocytic leukemia (CLL) disease, or for identifying agents that are useful in the therapy of CLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Fig 9B; 35pp; English.
                                                                                                                                                                                                                                            10-DEC-2001; 2001WO-US047931.
                                                                                                                                                                                                                                                                                        08-DEC-2000; 2000US-0254113P.
                                                                                                                                                                                                                                                                                                                                     (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                 Mcwhirter J;
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-599775/64.
                                                                                                                                                        WO200259280-A2
                                                                                                                                                                                                    01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                             Bowdish KS,
       Region
                                                                   Region
```

Gaps . 100.0%; Score 25; DB 5; Length 61; 100.0%; Pred. No. 53; 0; Indels 0; Mismatches Query Match
Best Local Similarity 100.
Matches 6; Conservative Sequence 61 AA;

ó

1 ASESIS ASESIS à

ABB79661 standard; protein; 61 AA. 21-OCT-2002 (first entry) ABB79661; RESULT 9 ABB79661 

Chronic lymphocyte leukaemia specific scrv F2d CDR sequences.

ö

Gaps

; 0

100.0%; Score 25; DB 5; Length 61; 100.0%; Pred. No. 53; 0; Indels ive 0; Mismatches 0; Indels

1 ASESIS 6 ASESIS

δ ద

Chronic lymphocytic leukaemia; CLL; scFv; antibody; rabbit; complementarity determining region; CDR; diagnosis; therapy.

```
The present sequence comprises a summary of the complementarity determining regions (CDRs) of the light chain and heavy chain of the chronic lymphocytic leukaamia (CLL) specific rabbit serv antibody F2d. Antibody regions separating the CDRs in the scrv are not given in the sequence. Rabbit scrv antibodies (see ABB79657-81) for B-CLL-specific cell surface antigens were selected using antibody phage display and cell surface antigens were selected using antibody phage display and cell surface panning. The invention provides a CLL line, CLL-AAT, derived from a B-CLL primary line without immortalisation by Epstein-Barr virus. The cell line is used to generate antibodies useful in the diagnosis and/or treatment of CLL. Antibodies derived from recombinant libraries may be selected using CLL-AAT as bait to isolate antibodies on the basis of specificity. Single chain antibodies are of particular use as they remain standing of the present scrv antibodies are of particular binding activity. The binding of the present scrv antibody to primary human cells and cell lines was determined by whole cell BLISA as follows: CLL (primary tumours and CLL-AAT cell line) ++; normal, primary human B lymphocytes, +; non-Hodgkin's lymphoma cell line RL, -; Burkitt's lymphoma cell line Ramos, -; and human erythroleukaemia cell line FP-1, -. A short linker separates
                                                                                                                                                                                                                                                                                                      19. 61
| Tabel= HC-CDR3
| Incte= "heavy chain complementarity determining region 3"
                                                  ...11
|Tabel= LC-CDR1
|Tote= "light chain complementarity determining region 1"
                                                                                              2. .18
| Jabel = LC-CDR2
| Incte= "light chain complementarity determining region 2"
                                                                                                                                                                     label= LC-CDR3
note= "light chain complementarity determining region 3"
                                                                                                                                                                                                14. .48
| Tabel= HC-CDR2
| Incte= "heavy chain complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New chronic lymphocytic leukemia cell line (designated CLL-AAT), useful for studying, diagnosing or treating chronic lymphocytic leukemia (CLL) disease, or for identifying agents that are useful in the therapy of CLL disease.
                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Fig 9B; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-DEC-2000; 2000US-0254113P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                10-DEC-2001; 2001WO-US047931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcwhirter J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-599775/64.
                                                                                                                                                                                                                                                                                                                                                                               WO200259280-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bowdish KS,
                                  Key
Region
                                                                                                   Region
                                                                                                                                                      Region
                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                           Region
```

```
9905-0139463P

9905-0139760P

9905-0139760P

9905-0139899P

9905-0140653P

9905-0140653P

9905-0140623P

9905-0140623P

9905-014220P

9905-014220P

9905-014220P

9905-014220P

9905-014220P

9905-014232P

9905-014433P

9905-014508P

9905-014508P

9905-014508P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0145224P.
99US-0145276P.
99US-0145913P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9905-0145918P-9905-0145918P-9905-014638BP-9905-014638BP-9905-014738P-9905-0147302P-9905-0147303P-9905-0147303P-9905-0147303P-9905-0147303P-9905-0148319P-9905-0148319P-9905-0148568P-9905-0148568P-9905-0148568P-9905-0148568P-9905-0148568P-9905-0148568P-9905-0148684P-9905-01494368P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-01499426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-0149426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-01494426P-9905-0149446P-9905-01494446P-9905-0149446P-9905-0149446P-9905-0149446P-9905-0149446P-9905-0149446P-9905-0149446P-990
                      99US-0139460P.
99US-0139461P.
99US-0139462P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0149722P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 - 7UL - 1999)
02 - AUG - 1999)
02 - AUG - 1999)
03 - AUG - 1999)
04 - AUG - 1999)
05 - AUG - 1999)
05 - AUG - 1999)
06 - AUG - 1999)
06 - AUG - 1999)
                                                                                                                                                                                                        01-JUL-1999;
01-JUL-1999;
02-JUL-1999;
                                                                                                                                                                                                                                                                                    12-JUL-1999;
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                    Zea mays protein fragment SEQ ID NO: 20468.
                                         AAG18882 standard; protein; 85 AA
                                                                                                                                                                                                                                                                                                    9908-012180P-
9908-0123180P-
9908-0125788P-
9908-0126564P-
9908-0126564P-
9908-0126764P-
9908-0126764P-
9908-0126764P-
9908-013264P-
9908-013264P-
9908-013264P-
9908-013264P-
9908-013268P-
9908-013268P-
9908-013268P-
9908-013268P-
9908-0134719P-
9908-0134719P-
9908-013468P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9903-0139119P.
9903-0139452P.
9903-0139453P.
9903-0139492P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0139455P.
99US-0139456P.
99US-0139457P.
                                                                                                                                                                                                                                                                              25-FEB-2000; 2000EP-00301439
                                                                                            17-OCT-2000 (first entry)
                                                                                                                                                                                                   Zea mays subsp. mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1999;
24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
27-MAY-1999;
01-JUN-1999;
04-JUN-1999;
07-JUN-1999;
07-JUN-1999;
07-JUN-1999;
07-JUN-1999;
08-JUN-1999;
                                                                                                                                                                                                                                                                                                                                          23. WAR-1999;
25. WAR-1999;
29. WAR-1999;
06. APR-1999;
06. APR-1999;
08. APR-1999;
19. APR-1999;
23. APR-1999;
23. APR-1999;
23. APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
                                                                                                                                                                                                                          EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-1999
30-APR-1999
                                                                                                                                                                                                                                                     06-SEP-2000
                                                                  AAG18882;
                RESULT 10
AAG18882
```

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                    Zea mays protein fragment SEQ ID NO: 20467.
                                                                                                                                       990S-01218259.
990S-01231809.
990S-01254889.
990S-01254889.
990S-01267859.
990S-01267859.
990S-01282349.
990S-0138919.
990S-01305109.
990S-01305109.
990S-013188919.
990S-01318489.
990S-01324848.
990S-01324848.
990S-01324849.
990S-01324869.
990S-01342199.
990S-01342199.
990S-0134249.
990S-0134249.
990S-0134249.
990S-0134249.
990S-0134249.
990S-0134249.
990S-0134249.
990S-0134249.
990S-01394529.
990S-01394529.
990S-01394529.
990S-01394529.
                                                                                                                        25-FEB-2000; 2000EP-00301439
  17-OCT-2000 (first entry)
                                                                      Zea mays subsp. mays.
                                                                                                                                                05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
                                                                                       EP1033405-A2
                                                                                                                                                                                                                     16-APR-1999;
19-APR-1999;
                                                                                                                                                                                                                                                                                         04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                             18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
                                                                                                        06-SEP-2000
                                                                                                                                                                                                                                                                                                                                           4-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                             4-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                     4-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAY-1999
28-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7-JUN-1999
  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 3; Length 85; Similarity 100.0%; Pred. No. 78; 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG18881 standard; protein; 89 AA.
                        9908-01505669
9908-01505669
9908-01510668-
9908-01510668-
9908-01513039-
9908-01513039-
9908-01533070-
9908-01533070-
9908-01533070-
9908-0154038-
9908-0154038-
9908-01556689-
9908-01556689-
9908-01556689-
9908-01556689-
9908-01556689-
9908-01556689-
9908-01556689-
9908-0155688-
9908-01593309-
9908-01593310-
9908-01593310-
9908-01593310-
9908-01593310-
9908-01593310-
9908-01593310-
9908-01593310-
9908-016984-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
9908-01698-
99US-0149723P.
99US-0149929P.
99US-0149902P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0161992P.
99US-0161993P.
99US-0162142P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASESIS
                                                                                                                                                                                        20.5 SEP-1999
04-0CT-1999
06-0CT-1999
06-0CT-1999
08-0CT-1999
12-0CT-1999
13-0CT-1999
13-0CT-1999
14-0CT-1999
14-0CT-1999
14-0CT-1999
14-0CT-1999
                        23-AUG-1999;
25-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
30-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
32-SEP-1999;
32-SEP-1999;
33-SEP-1999;
33-SEP-1999;
34-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG18881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
AAG18881
ID AAG180
XX
AC AAG180
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ଚ
```

99US-0139763P.

```
Single chain antibody; scFv; monoclonal antibody; MAb; 48-127; trop-2; gp54; antigen; cancer marker; bladder cancer; breast cancer; cervix cancer; prostate cancer; metastasis; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-gp54 MAb 48-127 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW26795 standard; protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; S.
ilarity 100.0%; P.
Conservative 0;
                 99105-0151303P

99105-0151430P

99105-015130P

99105-0153070P

99105-0154018P

99105-0154018P

99105-0154029P

99105-0154029P

99105-0155466P

99105-0155466P

99105-0155466P

99105-0155466P

99105-0155466P

99105-0155466P

99105-0155468P

99105-015833P

99105-015833P

99105-0159331P

99105-0159331P

99105-0159331P

99105-0159331P

99105-0159331P

99105-0159331P

99105-015933P

99105-015933P

99105-015933P

99105-015933P

99105-0160991P

99105-0161920P

99105-0161920P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 ASESIS 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASESIS
27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
10-SEP-1999;
11-SEP-1999;
12-SEP-1999;
20-SEP-1999;
20-SEP-1999;
20-SEP-1999;
20-SEP-1999;
20-SEP-1999;
20-SEP-1999;
20-SEP-1999;
20-SEP-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
22-OCT-1999;
23-OCT-1999;
23-OCT-1999;
24-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW26795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

99US-0133817P.
99US-0140393P.
99US-0140354P.
99US-0140354P.
99US-0140391P.
99US-0140391P.
99US-0142803P.
99US-0142803P.
99US-0142803P.
99US-0142803P.
99US-0142803P.
99US-0142803P.
99US-014332P.
99US-0144334P.
99US-0144334P.
99US-0144334P.
99US-0144334P.
99US-0144334P.
99US-0144334P.
99US-0144334P.
99US-0144334P.
99US-0144334P.
99US-0145913P.
99US-0145913P.
99US-0145088P.
99US-014508P.

\$\;\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\fr

. 0

Gaps ..

Indels

990S-0149722P. 99US-0149723P. 99US-0149929P. 99US-0149902P.

03-AUG-1999 04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999 10-AUG-1999 10-AUG-1999 10-AUG-1999

11-AUG-1999; 12-AUG-1999; 13-AUG-1999; 13-AUG-1999; 16-AUG-1999; 17-AUG-1999;

Mus sp. Region Region Region

```
The present sequence represents the light chain variable domain of murine monoclonal antibody 14E1. This antibody is active against the human epidermal growth factor receptor (EGF-R). The sequence is used to construct a single-chain polypeptide (soFv) that has binding affinity for an EGF-R. The scrv comprises two segments which contain the binding parts of the heavy and light chain variable domains of the monoclonal antibody 14E1. The scrvs of the invention are used to treat carcinomas (gliomas, melanomas and tumours) that overexpress EGF-R, specifically EGF-RvIII, relative to normal cells, particularly by blocking proliferation of such cells by preventing receptor activation. They can also be used for in vitro purging. When the scFV is appropriately labelled, it can be used diagnostically to image cells that express EGF-R, specifically breast
                                                                                                                                                                                                                                                                                                                    New single chain polypeptide that binds to epidermal growth factor receptor - is derived from antibody 14E, used for treatment and diagnosis of cancer or other cell proliferative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppression; tissue transplantation; graft; L chain; V region;
T-helper cell inhibition; transplant rejection; MAb;
interleukin-2 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-IL2R beta antibody MAb A41 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 2; Length 106; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                        Schneider DW;
                                                                                                                                                                                                                      Vakalopoulou E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR32129 standard, protein, 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 11D; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .96
/label≂ V-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97. .107
/label= J-region
                                                                                                 98WO-IB000413
                                                                                                                                         97US-00800198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                    Wels WS, Schmidt M,
                                                                                                                                                                                                                                                         WPI; 1998-467176/40.
N-PSDB; AAV54788.
                                                                                                                                                                              (SCHD ) SCHERING AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 ASESIS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 106 AA;
                      WO9836074-A2
                                                                                                 13-FEB-1998;
                                                                                                                                         13-FEB-1997;
                                                              20-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE4143214-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-2003
02-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR32129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
AAR32129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ношо
    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This polypeptide comprises the light chain variable region of murine monoclonal antibody (MAb) 48-127. This MAb recognises an epitope of gp54 antigen (trop-2), a cancer marker expressed at the surface of bladder, breast, uterine and prostate cancers. MAb 48-127 (IgG1) reacts with a majority of human bladder cell lines and with human breast carcinoma cell lines. The invention relates to novel single chain antibody (scFv) molecules, including a 48-127 scFv (see AAM2679) that comprises the 48-127 VH and VL chains joined via a linker. Such scFvs can be used to detect cancers and micromecastases, e.g. bladder, prostate, breast or uterine cervix cancers, and may be linked to specific toxins for use in cancer therapy. The scFvs are not immunogenic and are distributed and captured by 9P45-bearing target cells more quickly than conventional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant antibodies to gp54 antigen - used for the detection of cancers and metastases and for therapy of cancers expressing the gp54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment; carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 2; Length 104; 100.0%; Pred. No. 99; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain variable domain; antibody 14E1;
human epidermal growth factor receptor; EGF-R; tre
EGF-RvIII; in vitro purging; breast carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Light chain variable domain of antibody 14E1.
                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW71241 standard; protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 2; 33pp; English.
                                                                                                                                     47. .54
/label= CDR2
76. .84
/label= CDR3
                                                                                                                CDR1
                                                                                                                                                                                                                                                                                                                                                     96US-0026320P
                                                                                                                                                                                                                                                                                                               9.7WO-CA000690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                 21. .31
/label= (
                                                                                                                                                                                                                                                                                                                                                                                          (DIAG-) DIAGNOCURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Fradet Y, Darveau A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-217211/19.
N-PSDB; AAV26766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASESIS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 104 AA;
immunotherapy
                                                                                                                                                                                                                                                                                                             19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                   19-SEP-1996;
                                                                                                                                                                                                                                  WO9812227-A1
                                                                                                                                                                                                                                                                        26-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW71241;
```

antigen,

Mus sp.

RESULT 13

à

ö

Gaps

.; 0

```
ö
                                                                                                                                                                                                                                                                         This sequence is the light chain variable region of a preferred anti-IL2R beta monoclonal antibody for use in the claimed synergistic composition. The anti-IL2R beta antibody is used with at least one anti-CD4 antibody. Individually the antibody served with inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response. See AAQ36607-C36616. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                   Synergistic antibody compsn. for use as immunosuppressant - comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-IL2R beta antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity-determining region; CDR; humanised; antibody; hIL2R; human; interfleukhn; IL-2; receptor; mutine; anti-human; Ab; T-cell; monoclonal antibody; B-l0; mixed lymphocyte reaction; variable; V; region; PCR; framework; plasmid; heavy; H; light; L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 25; DB 2; Length 107; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                               Riethmueller G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR37610 standard; protein; 107 AA.
                                                                                                                 Weidle U, Scheuer W, Kaluza B,
                                                                                   (BOEF ) BOEHRINGER MANNHEIM GMBH
                                                                                                                                                                                                                                                 Claim 8; Page 17; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91JP-00323319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SUMU ) SUMITOMO PHARM CO LID. (BIOT ) BIOTEST PHARMA GMBH.
                          91DE-04143214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92WO-JP001583
                                                        91DE-04124759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B-B10 MAb L chain V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INNO-) INNOTHERAPIE LAB.
                                                                                                                                             WPI; 1993-037582/05.
N-PSDB; AAQ36615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 ASESIS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 107 AA;
                          30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-1991;
                                                        25-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9311238-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
13-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1993
28-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR37610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

Wijdenes J, Noguchi H;

Gomi H,

Nakatani T,

WPI; 1993-197057/24

6, 2004, 16:29:48

completed: October me : 32.3158 secs

Job time

Search

```
The sequences given in AAR37609-10 represent the heavy (H) and light (L) chain variable (V) regions of the murine anti-human IL-2 receptor monoclonal antibody (MAD) B-10, respectively. This MAD was used in the construction of a humanised antibody (AD) which binds specifically to human interleukin (IL)-2 receptor (HIL2R). The complementarity-catermining regions (CDRs) for the hIL2R MAD were derived from B-110 (see also AAR37599-04). The hIL2R MAD is antagonistic to the binding of IL-2 to the IL-2 receptor on human T-cells. It also inhibits the human mixed lymphocyte reaction. The CDNA encoding the variable (V) region of ILe B-110 V region CDR and a sequence (see also AAQ43226-32 and AAQ43233-36) A human Ab with high levels of amino acid sequence homology to the murine sequence was selected and the framework of this Ab was bound with this of the humanised B-110 V region. The DNA sequence coding this humanised B-110 W region. The DNA sequence coding this humanised B-110 was synthesised and a plasmid expressing humanised B-110 was constructed. (Updated on 25-MAR-2003 to correct PN field.)
                                       Humanised antibody comprising - CDR region of mouse MAB B-B10 specific for IL-2 receptor useful for treating carcinoma expressing IL-2 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 2; Length 107; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
                                                                                                                  Disclosure, Fig 2, 62pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 ASESIS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ASESIS 6
N-PSDB; AAQ43243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
```

us-09-635-974a-10.rsp

```
2
24
                                                                                                                                                                                                                                                                                                                    homo sapien
homo sapien
saccharomyc
chlamydia m
drosophila
                                                                                                                                                                                                                                                                                                                                                                                          salmonella
salmonella
neisseria g
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                               kennedya ye
pasteurella
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clostridium
escherichia
acinetobact
                                                                                                                                                                                                                                                                                  P01690 oryctolagus
P01642 mus musculu
P26213 aspergillus
                                                                                                                                                                                                                                                                                                                                                        neisseria g
chlamydia t
                                                                                                                                                                                                                                                                                                                                                                             lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                    homo sapien
                                                                                                                                                                                                                                                                                                  aspergillus
                                                                                                                                                                                                                                                                                                                                                                       homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                               oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                  tropheryma
bacillus su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmodium
                                             6, 2004, 16:21:13; Search time 3.68421 Seconds (without alignments) 84.800 Million cell updates/sec
                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                       141681
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                           141681 segs, 52070155 residues
                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                               S DROVI
NEIGO
T CHLTR
L HUMAN
L LACLA
L LACLA
SALTI
SALTY
                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                - protein search, using sw model
                                                                                                                                                                                                                                                                                          MOUSE
ASPNG
STRCO
STRAW
                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYMVJ
                                                                                                                                                                                                                                                                                                                                  YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                   CV15 HUMAN
                                                                                                                                                                                                                                                                                   RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                HSCA_
                                                                        US-09-635-974A-10
25
                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                       SwissProt_42;*
                                                                                                                                                                                                                                                       %
Query
Match Length D
                                                                                       1 ASESIS 6
                                               October
                                                                         Title:
Perfect score:
                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                  OM protein
                                                                                                                                                                                                     Database :
                                                                                       Sequence:
                                                                                                                          Searched:
                                              Run on:
                                                                                                                                                                                                                                                             Result
No.
```

| 068897<br>000233<br>000233<br>000233<br>000233<br>000233<br>000233<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>000023<br>000023<br>000023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00023<br>00 |                                                                                                                                                                                                                                                                 | Vertebrata; Euteleostomi;<br>e; Oryctolagus.<br>rg A.D., Haber E.;<br>n sequences among rabbit<br>";<br>Eu FROM ANTIBODY TO TYPE I<br>E SERUM OF A SINGLE RABBIT | DETERMINING-1. DETERMINING-2. DETERMINING-3.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | .; Length 92;<br>0; Indels 0; Gap                                                                  | ent).                                                                                                                                                      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 88.0 362 1 ASPG PSEFL<br>88.0 397 1 GDN MOUSE<br>88.0 414 1 XM42 MYCTU<br>88.0 427 1 ARP3 SCHPO<br>88.0 427 1 ARP3 SCHPO<br>88.0 432 1 CLPX CLOAB<br>88.0 433 1 HISX ECOS<br>88.0 433 1 HISX ECOL<br>88.0 446 1 NUAM DROYA<br>88.0 452 1 YEDV ECOLI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ULT 1  KV09 RABIT STANDARD, PRT; 92 AA. P01650; 21-UJL-1986 (Rel. 01, Created) 21-UJL-1986 (Rel. 01, Last sequence update) 15-UJL-1998 (Rel. 38, Last annotation update) 15-UJL-1999 (Rel. 38, Last annotation update) 19 kappa chain V region 3381 (Fragment). | craniata; Leporida 56; St. Strosbe able region e antigens 72.2180.21 WAS. OBTA-IN                                                                                | HASP: MOLISS; KNEAS. HIST: MOLISS; KNEAS. HIST: MOLISS; KNEAS. HIST: MORONIIO; IG-like. HIST: MORONIIO; IG-like. MART; SMOONOS; IGV: 1. MART; MOONOS; | 100.0%; Score 25; DB 1<br>.arity 100.0%; Pred. No. 4.9;<br>.onservative 0; Mismatches<br>.IS 6<br> | STANDARD; PRT; 115 AA. (Rel. 01, Created) (Rel. 01, Last sequence update) (Rel. 42, Last annotation update) in V-V region L7 precursor (Fragment) (Mouse). |
| 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | in 0                                                                                                                                                                                                                                                            | •                                                                                                                                                                | DER HSSP, A01593, DER HSSP, DO16073, DER INTERPRO, IPRR DER PERON | Query Match Best Local Similar Matches 6; Cor Oy 1 ASBSIG Db 25 ASBSIG                             | KESULT 2 KV51 MOUSE 1D - KV51 MOUSE 1D - LV51 MOUSE DT 21-UUL-1986 (Re DT 21-UUL-1986 (Re DT 10-CCT-2003 (Re DE 19 KAPPA OS MUS MUSCULUS ()                |

```
EMBL; AL939110; CAC12931.1; ALT_INIT. HAMAP; MF_00195; -; 1.
                                                                                                                            18 PO
31 PO
368 PO
229 PR
246 N-
38108 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
                                                                                                                             1
19
32 3
229 2
246 2
                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                     43 ASESIS 48
                                                                                                                                                                                                                                   1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                   ENGA STRCO
Q9EWW8;
                                                                                                                                                         ACT SITE
                                                                                                                                                                                               Query Match
                                                                                                                                                                            SEQUENCE
                                                                                                                                        PROPEP
CHAIN
                                                                                                                             SIĞNAL
                                                                                                                                                                                                                                                                                           ENGA_STRCO
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                RESULT
ઠે
                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                  ·:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=81220975; PubMed=6264318; MEDLINE=81220975; PubMed=6264318; Pech M., Hochtl J., Schnell H., Zachau H.G.; Pech M., Hochtl J., Schnell H., Zachau H.G.; Pifferences between germ-line and rearranged immunoglobulin V kappa coding sequences suggest a localized mutation mechanism."; Nature 291:668-670(1981).
                                                                                         -!- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICE JUNCTIONS 1 THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN LACKING RESIDUES 17-19.
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus niger.

Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes;

Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.

NCBI_TaxID=5061;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                   ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2, Last sequence update)
2, Last annotation update)
precursor (EC 3.2.1.15) (PG-I) (Pectinase)
                                                                                                                                                                                                                          IG KAPPA CHAIN V-V REGION L7.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 1; Length 115; 100.0%; Pred. No. 6.2; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING-3. BY SIMILARITY.
                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING-2
                                                                                                                                                                                                                                                                                                     115
12615 MW; C17BEC758C577E00 CRC64;
                                                                                                                                                                             pfam; PF60047; ig; i. --
SMART; SM0406; IGv; l.X.
SMO406; IG Like; 1.
Immunoglobulin V region; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                      368 AA
                                                                                                                                                                                                                                                                           FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-1992 (Rel. 22, Created) 01-WAY-1992 (Rel. 22, Last seqn 10-OCT-2003 (Rel. 42, Last anno Polygalacturonase I precursor
                                                                                                                               PDB; 1J10; 18-FEB-03.
PDB; 1J1P; 18-FEB-03.
PDB; 1J1X; 18-FEB-03.
ILLEFPC; IPR007110; IG-like.
InterPro; IPR003596; IG-V.
                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                             >115
                                                                                                                                                                                                                                                                                             43 1
115 1
115 AA;
                                                                                                                         A01925; KVMSL7
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    71 ASESIS 76
                                                                                                                                                                                                                                                                                                                                                                       1 ASESIS 6
                   NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PGL1_ASPNG
P26213;
                                                                                                                                                                                                                                                                                             DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                   Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                             EMBL; X58892; CAA41693.1; -.
PIR; S17980; S17980.
InterPro; IPR000743; Dilycohydro_28.
InterPro; IPR000626; PbHI.
Pfam; PF00295; Glycohydro_28; 1.
SMART; SW00710; PbHI; 6.
PROSTIF; PS00502; POLYGALACTURONASE; 1.
Hydrolase; Glycosidase; Cell wall; Signal; Zymogen; Multigene family; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE 21996410; PubMed=12000953; Bentley S.D., Challis G.L., Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Eraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch B., Rajandream M.A., Rutherford K., Futter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE.
N-LINKED (GLCNAC. . .) (PROBABLE)
CD9846A9A99B5102 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: GTPase of unknown physiological role. -!- SIMILARITY: Belongs to the era/trmE family of GTP-binding proteins. EngA subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 1; Length 368; 100.0%; Pred. No. 23; 0; Indels iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. POLYGALACTURONASE I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-FAR-2004 (Rel. 43, Last annotation update)
GTP-binding protein engA.
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SETALINAA-4660 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

MEDLINE=22608306; PubMed=12692562;

Ikeda H., Ishikawa J., Hananoco A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;

"Complete genome sequence and comparative analysis of the industrial

"Complete genome Sequence and comparative analysis of the industrial

microorganism Streptomyces avermittiis.";

Nat. Biotechnol. 21:526-531(2003):

I- FUNCTION: GTPase of unknown physiological role.

-I- SIMILARITY: Belongs to the era/trmE family of GTP-binding

proteins. EngA subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; Pubmed=11572948;
Omura S., Ikeda H., Ishkawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hatchori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
metabolites."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces avermitilis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 1; Length 465; 100.0%; Pred. No. 30; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           GTP 1 (POTENTIAL).
GTP 1 (POTENTIAL).
GTP 1 (POTENTIAL).
GTP 2 (POTENTIAL).
GTP 2 (POTENTIAL).
GTP 2 (POTENTIAL).
GTP 2 (POTENTIAL).
M, 9E053E7C00C859F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        491 AA
                  InterPro; IRR005899; GTP-bindding_dom.
InterPro; IRR005899; GTP-bindding_dom.
InterPro; IRR005891; GTP-10BG.
InterPro; IRR002917; MRR EGRI.
InterPro; IRR002917; MRR EGRI.
InterPro; IRR00225; Small_GTP.
Pram; Pr00326; GTP10BG.
SMART; SM00382; AAA, 2.
IGRRAMS; TIGR00650; MG442; 2.
IGRRAMS; TIGR00650; MG442; 2.
IGRRAMS; TIGR00231; Small_GTP; 2.
GTP-binding; Repeat; Complete proteome.
NP_BIND 38 40 GTP 1 (POTEW NP_BIND 142 145 GTP 1 (POTEW NP_BIND 208 215 GTP 2 (POTEW NP_BIND 208 213 GTP 2 (POTEW NP_BIND 208
   AAA_ATPase.
GTP-bindding_dom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP-binding protein enga.
ENGA OR SAV6524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 ASESIS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
ENGA_STRAW
ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
MEDLINE=22050606; PubMed=11929878;

MEDLINE=22050606; PubMed=11929878;

LOFE., Hong W.;

Todgi and exists in a complex with GTC-90 and IdlBp.";

Golgi and exists in a complex with GTC-90 and IdlBp.";

J. FINCTICAN: Involved in ER-6019; Lanssport.

C. I- SUBUNIT: Component of the conserved oligomeric Golgi complex which is composed of stipt different subunits and is required for normal Golgi morphology and localization (By similarity).

C. SUBCELLUIAR LOCATION: Golgi. Associated with the peripheral membrane of cisfmedial cisternae.

C. SUBCELLUIAR LOCATION: Golgi. Associated with highest levels in pancreas and testis and lowest levels in lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21303883; PubMed=11292827; Suvorova E.S., Kurten R.C., Lupashin V.V.; Indentification of a human ortholog of Sec34p as a component of the cis-Golgi vesicle tethering machinery."; J. Biol. Chem. 276:22810-22818 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0960B2; 09B292;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
20-FBB-2003 (Rel. 41, Last annotation update)
20-FBB-2003 (Rel. 41, Last complex component 3 (Vesicle docking protein SEC34 homolog) (p94).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 1; Length 491; 100.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7BADD8E0449D14AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                       te proteome.
GTP 1 (POTENTIAL).
GTP 1 (POTENTIAL).
GTP 2 (POTENTIAL).
GTP 2 (POTENTIAL).
GTP 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                       HAMAP, MF 00195; -; 1.
InterPro, IPR003593; AAA ATPase.
InterPro, IPR005289; GTP-bindding_dom.
                                                                                                  InterPro; IPRO0223; GIT-LINGALING-GOS
INTERPO; IPRO02217; MWR HSR1.
INTERPO; IPRO0225; Small GTP.
PRAM: PPO1926; MWR HSR1, 1.
PRINTS; PRO0326; GTPLOBG.
SWART; SMO0382; GTPLOBG.
IIGRPAMS; TIGRO050; MG442; 2.
TIGRPAMS; TIGRO051; Small GTP; 2.
GTP-binding; Repeat; Complete Protect
NP_BIND 166 110 GTP 1 (NP_BIND 168 171 GTP 1 (NP_BIND 168 171 GTP 2 (NP_BIND 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 ASESIS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
COG3 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              요
```

ò 원

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=S2862 / AB972;
MEDLINE=9313266; PubMed=9169870;
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelron J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
Withe nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
Nature 387:84-87(1997).
                                                                                                                                                                                                         MALT, 1,730.3, C:endosome, TAS.

GO; GO:0005862; C:intermediate filament; TAS.

GO; GO:0005862; C:intermediate filament; TAS.

GO; GO:0006862; C:intermediate filament; TAS.

GO; GO:0008017; F:microtubule binding; TAS.

GO; GO:0006899; P:nonselective vesicle transport; TAS.

InterPro; IPR000938; CAP-GIY.

InterPro; IPR001938; CAP-GIY.

InterPro; IPR001938; CAP-GIY.

SWART; SW00343; ZAP-GIY: 2.

SWART; SW00343; ZAP-GIY: 1; 2.

PROSITE; PS50246; CAP-GIY: 2.

CYtoskeleton; Microtubule; Coiled coil; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical 56.3 kDa protein in SGAl-KTR7 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 1; Length 1427; llarity 100.0%; Pred. No. 1e+02; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1408 1421 CCHC-BOX.
457 491 Missing (in isoform Short).
//TIG=VSP 000765.
1069 D -> E (IN REF. 2).
1427 AA, 160989 MW; 0A4F166DD94254E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAP-GLY 1.
SER-RICH.
CAP-GLY 2.
SER-RICH.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                           EMBL, X64838, CAA46050.1, -...
EMBL, M97801, AAA35693.1; -...
PIK, S22695, S22895.
GGBGW, HGNN:10461; RSN.
MIM, 179838; --...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 ASESIS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YIJO YEAST
P40499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RWBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name-Short;
IsoId=P30622-2; Sequence=VSP_000765;
mrsorm cDRCIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED PROTEIN THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES. SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Peripheral blood monocytes;
MEDLINE=92289675; PubMed=1600942;
Bilbe G., Delabie J., Brueggen J., Richener H., Asselbergs F.A.M.,
Cerletti N., Sorg C., Odink K., Tarcsay L., Wiesendanger W.,
de Wolf-Peeters C., Shipman R.;
"Restin: a novel intermediate filament-associated protein highly
expressed in the Reed-Sternberg cells of Hodgkin's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-PBB-2003 (Rel. 41, Last annotation update)
Restin (Cytoplasmic linker protein-170 alpha-2) (CLIP-170) (Reed-sternberg intermediate filament associated protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 1; Length 828; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                    Jenew; HGNC....

MIM; 606975; --
Interpret; IPR007265; Sec34.

Pfan; PF04136; Sec34; 1.

Transport; Protein transport; Golgi stack; Membrane.

Transport; Protein transport; HE -> QQ (IN REF. 2).

CONFLICT 106 107 HE -> QQ (IN REF. 2).

747 N -> SG (IN REF. 2).

Tangth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92405160; PubMed=1356075;
Pierre P., Scheel J., Rickard J.E., Kreis T.E.;
"CLIP-170 links endocytic vesicles to microtubules.";
Cell 70:887-900(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 2 CAP-Gly domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P30622-1; Sequence=Displayed;
                                            entities requires a license agreement (6
or send an email to license@isb-sib.ch)
                                                                                                                           EMBL; AF349676; AAK66974.1; -.
                                                                                                                                              EMBL; AF332595; AAK06848.1; -. Genew; HGNC:18619; COG3.
                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: H
OF HODGKIN'S DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASESIS 600
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOSKELETON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REST HUI
P30622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7

REST HUMAN

REST HUMAN

AC 11-APR-
DD 1 28-FEB-
DD REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST DD

REST
```

ö

Gaps

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                DOMAIN
METAL
                                                                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOSS_DROVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A White O., Hickey E. K., Peterson J., Utterback T., Berry K., Bass S.,
A White O., Hickey E. K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Bisen J., Fraser C.M.;
T. "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
Dneumoniae AR39.";
I wucleic Acids Res. 28:1397-1406 (2000).
- CATALYTIC ACTIVITY: ATP + L-throonine + tRNA(Thr) = AMP +
diphosphate + L-throonyl-tRNA(Thr).
- CATALYTIC ACTIVITY: ATP + L-throonine + CRNA(Thr) = AMP +
- CATALYTIC ACTIVITY: ATP + L-throonine + CRNA(Thr) = AMP +
- CATALYTIC ACTIVITY: ATP + L-throonine + CRNA(Thr).
- CATALYTIC ACTIVITY: ATP + L-throonine + CRNA(Thr).
- CORPACTOR: Binds 1 zinc ion per subunit (By similarity).
- SUBCELLULAR LOCATION: Cytoplasmity).
- SUBCELLULAR LOCATION: Cytoplasmity).
- SUBCELLULAR LOCATION: Cytoplasmity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia muridarum.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.0%; Score 24; DB 1; Length 491; 83.3%; Pred. No. 62; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  BAEC655534E04239 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          635 AA
                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MoPn / Nigg;
MEDLINE=20150255; Pubmed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AE002353; AAF39666.1; -. PIR, A81656; A81656. HSSP, P00955; TEVL. TICR; TC0870; -. HAMAP; MF_00184; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    56332 MW;
                                           EMBL; Z46728; CAA86704.1; -. PIR; S49790; S49790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                 GermOnline, 139625, -. SGD, S0001352, YIL090W. Hypothetical protein, T
                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 ASESVS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                  491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THRS OR ICO870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHLMU
                                                                                                                                                                           TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYT CHLM
Q9PJF9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYT_CHLMU
SPETT FETT FETT SOLUTION SOLUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
InterPro; IPR004154; HGTP anticodon.
InterPro; IPR004055; TGS dow.
InterPro; IPR002320; TRNA-SYNT 2b.
InterPro; IPR002320; TRNA-SYNT 2b.
InterPro; IPR002320; TRNA-SYNT 2b.
InterPro; IPR006435; TRNA-Ligase_II.
Pfam; PF03824; TGS; lanticodon; l.
PRINTS; PR0806418; thrS; l.
TIGRFAMS; TIGR00418; thrS; l.
TIGRFAMS; TIGR00418; thrS; l.
Aminoacyl-ERNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Aminoacyl-ERNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93281693; PubMed=8506350; MEDLINE-93281693; PubMed=8506350; MEDLINE-93281693; PubMed=8506350; MEDLINE-93281693; PubMed=8.0. van Vactor D.L. Jr., Rubin G.M., Zipursky S.L.; Whe interaction of bride of sevenless with sevenless is conserved between Drosophila virilis and Drosophila melanogaster."; Proc. Natl. Acad. Sci. U.S.A. 90:5047-5051(1993).

-I. FUNCTION: Acts as a ligand for sevenless tyrosine-kinase receptor during eye development.

-I. SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila virilis (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZINC (CATALYTIC) (BY SIMILARITY)
ZINC (CATALYTIC) (BY SIMILARITY)
ZINC (CATALYTIC) (BY SIMILARITY)
39825894E70521AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.0%; Score 24; DB 1; Length 635; 83.3%; Pred. No. 82; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Glycoprotein; Vision; Signal.
SIGNAL
1 30 POTENTIAL.
CHAIN 32 BRIDE OF SEVENLESS PROTEIN.
DOMAIN 32 530 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOSS_DROVI STANDARD; PRT; 893 AA. 024738; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) Bride of sevenless protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L08132; AA72332.1; -.
PIR; A47550; A47550.
FlyBase; FBgn0013105; Dvir\boss.
InterPro; IPR002956; Bride of 7less.
InterPro; IPR000337; GPCR Mgr.
Pfam; PF00003; 7tm_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01223; BRIDEOF7LESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328
379
505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328
379
379
505
635 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||:|
568 ASESVS 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HERE THE PROPERTY OF THE PROPE
```

φ

```
DORRANDO REPTETATOR
                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: THE SIGNAL PEPTIDE GUIDE THE PRECURSOR TO THE PERIPLASMIC SPACE, AND THE CARBOXY-TERMINAL HELDER DOMAIN ASSOCIATES WITH THE OUTER MEMBRARE TO FORM A PORE FOR EXCRETION OF THE PROTEASE DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTECLYSIS.
-!- SIMILARITY: Belongs to peptidase family $6.
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-87115823; PubMed=3027577;
Pohlner J., Halter R., Beyreuther K., Meyer T.F.;
"Gene structure and extracellular secretion of Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=90154052; PubMed=2105953; Bachovchin W.W. Plaut A.G., Flentke G.R., Lynch M., Kettner C.A.; Enchotchin with Plaut A.G., Flentke G.R., Lynch M., Kettner C.A.; Inhibition of IgAl proteinases from Neisseria gonorrhoeae and Hemophilus influenzae by peptide prolyl boronic acids."; J. Biol. Chem. 265:3738-3743(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U. Biol. Chem. 265:3738-3743(1990).
-!- FUNCTION: THIS PROTEASE IS SPECIFIC FOR IMMUNOGLOBULIN A.
-!- CATALYTIC ACTIVITY: Cleavage of immunoglobulin A molecules at certain Pro-|-Xaa bonds in the hinge region. No small molecule
                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last amocation update)
IgA-specific serine endopeptidase precursor (EC 3.4.21.72) (IgA
                                                                                                            CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL)

                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria gonorrhoeae.
Bacteria; Próteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                               Score 24; DB 1; Length 893;
Pred. No. 1.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                     99939 MW; ABB9D4C21DB680C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1532 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN=MS11;
                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
                                            POTENTIAL.
                                                          POTENTIAL.
 POTENTIAL
                              POTENTIAL
                                                                                                                                                                                                                                 96.0%;
                                                                                                                                                                                                                   Query Match
Best Local Similarity 83...
From 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  substrates are known.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 325:458-462(1987)
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                      712
742
772
772
772
893
307
471
                                                                                                                                                                                                                                                                                                                     676 ASESVS 681
                                                                                                                                                                                                     893 AA;
                                                                                                                                                                                                                                                                                         1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IgA protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVE SITE.
                                                                                                                                                                                                                                                                                                                                                                                           IGA NEIGO
P09790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protease).
                                                                                                 TRANSMEM
DOMAIN
CARBOHYD
TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                         CARBOHYD
CARBOHYD
                                                                                                                                                                                       CARBOHYD
SEQUENCE
                                          TRANSMEN
                                                           TRANSMEM
                                                                                    TRANSMEM
                                                                                                                                            CARBOHYD
                                                                       IRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                           8
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=D/UW-3/Cx;
MEDILIDE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 282:754-759(1998).
-!- SIMILARITY: Belongs to the chlamydial CPn0441/CT007/TC0275 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                    IGA-SPECIFIC SERINE ENDOPEPTIDASE.
HELPER PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                PRINTS; PR00921; IGASERPTASE.
TYGRRAM; TIGR01414; autotrans barl; 1.
Hydrolase; Serine protease; Zymogen; Autocatalytic cleavage;
Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24; DB 1; Length 1532;
Pred. No. 2.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      MW; 68FF4112BD22F40D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; F71569; B71569.
Hypothetical protein; Complete proteome.
SEQUENCE 316 AA; 35637 MW; 904D2CC28F5CB06E CRC64;
                                                                                                                                                                                                                                                                                                                                                                (AUTO-).
(AUTO-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
InterPro; IPR009003; Oya Ser_trypsin.
InterPro; IPR000110; Peptidase_S6.
InterPro; IPR000110; Peptidase_S6.
InterPro; IPR00084; TrpBP.
InterPro; IPR00084; TrpBP.
Ffam; PP03797; Autotransporter; 1.
Pfam; PP03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                CLEAVAGE (
CLEAVAGE (
CLEAVAGE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001275; AAC67597.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.0%;
EMBL; X04835; CAA28538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      168976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein CT007.
CT007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                   1121 112
1532 AA;
                   PIR; A26039; A26039.
MEROPS; S06.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1200 ASESVS 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Chlam
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y007 CHLTR
O84010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia
                                                                                                                                                                                                                                                                                                                                               ACT SITE SITE
                                                                                                                                                                                                                                                                                                                                                                                                   SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                            CHAIN
PROPEP
                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
```

Score 23; DB 1; Length 316; Pred. No. 73;

92.0%;

Query Match Best Local Similarity

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *** MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Collins F.S., Wagner L., Shamen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F.; Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scares M.B., Bromatein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketteman M., Madan A., Rothigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Hepatoma;
MEDLINE=22092308; PubMed=12097419;
Mang Y., Han K.-J., Pang X.-W., Vaughan H.A., Qu W., Dong X.-Y.,
Peng J.-R., Zhao H.-T., Rui J.-A., Leng X.-S., Cebon J., Burgess A.W.,
Chen W.-F.;
                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.

MEDLINEE20164601; PubMed=10699956;

MEDLINEE20164601; E., Arden K.C., Boyer A.D., Viars C.S.,

Gure A.O., Stockert E., Arden X.-T.;

Scanlan M.J., Old L.J., Chen Y.-T.;

"CT10: a new cancer-testis (CT) antigen homologous to CT7 and the MAGE family, identified by representational difference analysis.";

Int. J. Cancer 85:726-732(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=20321428; PubMed=10861452;
Lucas S., De Plaen B., Boon T.,
"MAGE-B5, MAGE-C2, and MAGE-C3: four new members of the MAGE
family with tumor-specific expression.";
Int. J. Cancer 87:55-60(2000).
   Gaps
                                                                                                                               MGEI HUMAN STANDARD; PRT; 3/3 AA.

909UBFi, OPPLMF; OPPLM;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Melanoma-associated antigen El (MAGE-El antigen) (MAGE-C2 antigen)
(Hepatocellular carcinoma-associated antigen 587) (Cancer-testis
                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-! TISSUE SPECIFICITY: Expressed in testis and in liver cancers.
-! SIMILARITY: Contains 1 MAGE domain.
   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Large scale identification of human hepatocellular carcinoma-
associated antigens by autoantibodies.";
J. Immunol. 169:1102-1109(2002).
   Indels
   .
0
 Mismatches
   ;
;
                                                                                                                                                                                                                                       antigen CT10).
MAGEE1 OR MAGEC2 OR HCA587.
5; Conservative
                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                          172 ASESLS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                             1 ASESIS 6
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                    HUMAN
   Matches
                                                                                                    RESULT 13
                             δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINEALIZESTES F. WHORGELISS. "AIL J. MEDLINEALIZESTES F. WHORGER P., Mancker P., Mancker P., Mancker P., Mancker P., Mancker P., Sorokin A.; Wincker P., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus acts sep. lactis ILI403 "The complete Res. 11:731-753(2001).
-! FUNCTION: Efflux transporter for a variety of amphiphilic cationic compounds, including antibiotics (By similarity).
-! SUBUNIT: Honodimer (Potential).
-! SUBUNIT: Honodimer (Potential).
-! SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBL_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Multidrug resistance ABC transporter ATP-binding and permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAGE.

POLY-GLU.

POLY-GLU.

SER-RICH.

SER-RICH.

K -> T (IN REF. 1; AAF34816).

K -> E (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    590 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 88;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%; Score 23;
83.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=111403;
MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                                 EMBL; AF116194; AAF34816.1; --
EMBL; AF116195; AAF34817.1; --
EMBL; AF196483; AAF07211.1; --
EMBL; AF151378; AAF07210.1; --
EMBL; AF151378; AAF36533.1; --
EMBL; AF239802; AAK15073.1; --
EMBL; BC005891; AAH0891.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen; PS50838; MAGE; 1.
Antigen; Multigene family.
DOWAIN 34 38
DOWAIN 40 60
DOWAIN 67 70
DOWAIN 82 118
CONFLICT 189 189 18
SEQUENCE 377 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002190; MAGE.
Pfam; PF01454; MAGE; 1.
PROSITE; PS50838; MAGE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:13574; MAGEE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 ASESLS 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMRA OR LL0711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
LMRA LACLA
ID LMRA LAC
AC Q9CHEB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

```
Search completed: October 6, 2004, 16:30:30 Job time : 6.68421 secs
                                                                                                                                                                                                                                                                                                                                                                        214 ASESLS 219
                                                                                                                                                                                                                                                         590 AA;
                                                                                                                                                                                                                                                                                                                                              1 ASESIS 6
                                                                                                                                         TRANSMEM
TRANSMEM
                                                                                                                                                                    TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                              DOMAIN
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                TRANSMEN
                                                                                                                                                                                                                                                                                                    Best Loc
Matches
 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWISL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license also removed. (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MC1363,
MEDLINE=97008061; PubMed=8855237;
Wan Veen H.W., Venema K., Bolhuis H., Oussenko I., Kok J., Poolman B.,
Driessen A.J., Konings W.N.; Bolhuis H., Oussenko I., Kok J., Poolman B.,
Multidrug reasistance mediated by a bacterial homolog of the human
multidrug reasisporter MRH1.";
Proc. Natl. Acad. Sci. U.S.A. 93:1068-10672(1996).
-!- FUNCTION: Efflux transporter for a variety of amphiphilic cationic
compounds, including antibiotics.
-!- SUBGNIT Homodimer (Potential).
-!- SUBGNIT Homodimer (Potential).
-!- SUBGNITHE LOCATION: Integral membrane protein (Probable).
-!- SUBGNITHE LOCATION Integral membrane protein (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1359;
                                                                                                                                                                                                                                                                                                                                                                                                    o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P97046;
28-FBB-2003 (Rel. 41, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Multidrug resistance ABC transporter ATP-binding and permease
                                                                                                                                                    PROSITE; PSS0929; ABC_TMIF; 1.
PROSITE; PSS0929; ABC_TRANSPORTER_1; 1.
PROSITE; PSS0839; ABC_TRANSPORTER_2; 1.
ATP-binding; Transport; Transmembrane; Antibiotic resistance; Complete proteome. 35 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                        Length 590;
                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 1; Length 590
Pred. No. 1.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                            8DF41419A01388CA CRC64;
                                                                                                                                                                                                                                                                                                 POTENTIAL.
ABC TRANSPORTER.
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  590 AA.
send an email to license@isb-sib.ch)
                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                     POTENTIAL.
                                                    InterPro; IPR003593; AAA_ATPase.
InterPro; IRR001140; ABC_TM transpt.
InterPro; IPR00140; ABC_TM transporter.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
ProDom, PD000006; ABC_tran; 1.
SMART; SM00382; AAA; 1.
                         EMBL; AE006305; AAK04809.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U63741; AAB49750.1; -.
InterPro; IPR003593; AAA_ATPase.
                                                                                                                                                                                                                                                                                                                                           64698 MW;
                                                                                                                                                                                                                                                                                                                                                                        92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                           SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||:|
214 ASESLS 219
                                        G86713; G86713
                                                                                                                                                                                                                                                                                                                                           590 AA;
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMRA LACLC
                                                                                                                                                                                                                                                                                                              DOMAIN
NP BIND
SEQUENCE
                                                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                     Interpro; IPR003439; ABC_transporter.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_membrane; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS50929; ABC_TRNIF; 1.
PROSITE; PS50929; ABC_TRNSPORTER_1; 1.
PROSITE; PS50893; ABC_TRNSPORTER_2; 1.
ATP-binding; Transport; Transmembrane; Antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 1; Length 590;
Pred. No. 1.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         CCE4E7D4EF912B8D: CRC64;
                                                                                                                                                                                                                                                                                                                                ABC TRANSPORTER. ATP (POTENTIAL).
                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
InterPro; IPR001140; ABC_IM transpt. InterPro; IPR003439; ABC_transporter
                                                                                                                                                                                                                                                                                                                                                                       64617 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              / Match 92.0%;
Local Similarity 83.3%;
nes 5; Conservative
```

Q9ugm5 homo sapien Q8ucm5 homo sapien Q8c056 mus musculu Q8dy17 streptococc Q8p3v6 xanthomonas Q8pfd5 xanthomonas Q8pfd5 xanthomonas Q9ue80 homo sapien Q9ue80 homo sapien Q9ue80 homo sapien Q9ue80 homo sapien Q9ue41 streptococc Q9jx25 rattus norv Q8ue41 homo sapien Q922j3 mus musculu Q27802 tripneustes Q9sen streptococc Q8a2v6 bacteroides Q9mrs0 corynebacte Q9mrs0 corynebactericity Q81909 drosophila Q81909 drosophila Q81909 drosophila Q9neus dictyostelicated

094462 0900MS 09010MS 0800MS 0800MS 0800MS 092656 092635 092635 091775 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 092633 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 09263 092

Q8T909 Q8IPW9 Q9VQ15 Q9NKW1 O21860

us-09-635-974a-10.rspt

```
C STRAIN=MARP301099;

K REDLINE=21082930; PubMed=11214968;

K KADELNE=21082930; PubMed=11214968;

K KADELNE=21082930; PubMed=11214968;

K KADELNE=21082930; PubMed=11214968;

KADELNE=21082930; PubMed=11214968;

KADELNE=21082930; PubMed=11214968;

KADELNE=21082930; PubMed=11214968;

KADELNE=21082930; Rohara A., Kawashima K., Kimura T.,

KADELNE A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto M., Matsuki Y., Nakayama S., Rakazaki N., Shimpo S., Sugimoto M.,

Takeuchi C., Yamada M., Tabata S.;

Takeuchi C., Yamada M., Yamad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Match 100.0%; Score 25; DB 16; Length 225; Local Similarity 100.0%; Pred. No. 87; es 6; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Phyllobacteriaceae, Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein mll5052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 ASESIS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
                                                 1 ASESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               098C02;
01-OCT-2001 (
01-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q98CQ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT

      11112
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222
      1222

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q98cq2 rhizobium 1
Q98cq2 rhizobium 1
Q99m54 mus musculu
Q8837 mus musculu
Q8837 mus musculu
Q88439 pseudomonas
Q7x6h5 oryza sativ
Q86fw4 homo sapien
Q86fw4 homo sapien
Q86fw4 homo sapien
Q86fw3 caenorhabdi
Q85aya streptomyce
Q32d8 staphylococ
Q343d8 staphylococ
Q34df prochloroco
Q7vdf7 prochloroco
Q7vdf7 prochloroco
Q7vdf7 prochloroco
Q7vdf7 prochloroco
Q7vdf7 prochloroco
Q7vdf4 prochloroco
Q7vdf4 prochloroco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                             6, 2004, 16:23:13 ; Search time 20:1053 Seconds (without alignments) 94.160 Million cell updates/sec
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1017041 segs, 315518202 residues
                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q98CQ2
Q99MS4
Q99MS4
Q98MS37
Q98K39
Q7X6HS
Q88KW4
Q98KW4
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_fungi:*
5: pinvertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                           US-09-635-974A-10
25
1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              October
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5:
77:
10:
10:
                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
No.
```

ö

Gaps

. 0

OO BONG OO BONG OO CON WAY OO CON

```
TISSUB-Embryo, Embryonic stem cells, and Small intestine;

TISSUB-Embryo, Embryonic stem cells, and Small intestine;

X Manal V., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X Axakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,

Azakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,

Azakawa T., Jawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azakawa T., Ashburner M., Bando H., Salto R.,

Radota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Beralov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pecole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pecole G., Quackenbush J.,

Schriml L., M., Staubli F., Suzuki R., Tomitca M., Wagner L., Washlo T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Winnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Rodriguez C., Wawaji H., Kohtsuki S.,

Nordone P., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
Chromosome 6 BAC-284H12 (RESEARCH GENETICS mouse BAC LIBRARY) complete sequence (RESEARCH GENETICS mouse BAC LIBRARY) (2410005A12RIK protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Muzny D., Ansari-Lari M.A., Timms K.M., Yu W., Dugan S., Lu J., Shen Y., Rowland K., Liu W., Perez L., Ding Y., Haywood M., Jain A., Leal B., Logan O., Nguyen V., Savage L., Shen H., Worley K., Chen E., Forcum J., Arenson A.D., Chiu M.W., Gorrell J.H., Brundage E., Di W., "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muzny D., Arenson A.D., Adams C., Brundage E., Bunac C., Carvelli K., Chacko J., Chen J., Di W., Ding Y., Dugan S., Durbin J., Forcum J., Ganesh R., Garcia C., Goodman M., Gorrell J.H., Haywood M., Hernandez J., Jackson L., Jin S., Kampal R., Karpathy S., Kovar C., Leal B., Li Y., Lichtearge O., Liu W., Logan O., Lu J., Ly T., Martinez C., Oswal G., Perez L., Rashid N.D., Rowland K., Savage L., Scher R. E., Shen H., Simon M., Stovall K., Timms K.M., Todd J., Gibbs. R.A.;
                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98112780; PubMed=9445485;
Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
Lu J., Gorrell J.H., Chinault A.C., Belmont J.W., Miller W.,
                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                        "Comparative sequence analysis of a gene-rich cluster at human chromosome 12p13 and its syntenic region in mouse chromosome 6.1; Genome Res. 8:29-40(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J;
MEDLINE=22354683; PubMed=12466851;
                                            (Gene rich cluster).
GRCC8 OR C8 OR 2410005A12RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
                                                                                                                                                                                                                                                                                     Lu J., Gorr
Gibbs R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Functional
    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                      STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                               Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 16; Length 248; 100.0%; Pred. No. 97; ive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 11; Length 266; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002006; AAH02006.1; -.
MGD; MGI:1315198; Grcc8.
SEQUENCE 266 AA; 28873 MW; BE0845BA96CF3C57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D74C9AA260DA049C CRC64;
                                                                  01-0CT-2001 (TrEMBLrel. 18, Created)
1-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0TT-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein MYPU_3250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                           248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma pulmonis.";
Mucleic Acids Res. 29:2145-2153(2001).
BNEL, AL445564; CAC13498.1;
PIR; E90552; E90552.
Mypulist; MYPU 3250;
Hypotheical protein; Complete proteome.
SEQUENCE 248 AA; 28555 MW; D74C9AA26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08837;
01-NOV-1998 (TEMBLEEL: 08,
01-NOV-1998 (TEMBLEEL: 08,
01-MAR-2003 (TEMBLEEL: 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rich cluster, C8 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 6; Conservative
                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 ASESIS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 ASESIS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                            Moszer I., Dyt
Blanchard A.;
                                                                                                                                                                   MYPU 3250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q99M54;
                      9N0860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             099M54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         088837
```

Gene

ò

RESULT 3
2099M54
10 0099M
AC 0999M
AC 0999M
AC 01-J
DT 
Matches

В

RESULT 4 088837 ID 0888: AC 0888: DT 01-N DT 01-N DT 01-N

```
Query Match
Best Local Similarity 100.00
Best ca 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 AA;
                                                                                                                                                                                                                                                                                                         91 ASESIS 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASESIS 30
                                                                                                                                                                                                                                                                                     1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              Q7X6H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                         RESULT 7
Q7X6H5
    ઠે
                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=cv. Stella d'Oro; TISSUE=Senescing petals;
MEDLINE=99339248; PubMed=10412903;
MEDLINE=99339248; PubMed=10412903;
Panavas T., Pikula A., Reid P.D., Rubinstein B., Walker B.L.;
"Identification of senescence-associated genes from daylily petals.";
Plant Mol. Biol. 40:237-248(1999).
HSSP; P24289; 1AKO.
                                                                                                          Gaps
                                                                                                                                                                                                                                                                        Hemerocallis sp. (Daylily).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales,
Hemerocallidaceae, Hemerocallis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 10; Length 298; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels (
                                                                                  100.0%; Score 25; DB 11; Length 266; 100.0%; Pred. No. 1e+02;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02265; Nuclease; 1.
SEQUENCE 298 AA; 34109 MW; 7FF90F476FFB0057 CRC64;
                                                    MGD; MGI:1315198; Grcc8.
SEQUENCE 266 AA; 28708 MW; BE02E77ACAAAC2F8 CRC64;
                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q08K39 PRELIMINARY; PRT; 362 AA.
BBRX39;
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
L-asparaginase II.
ANSA OR PP2453.
                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0004519; F:endonuclease activity; IEA. GO; GO:0003676; F:nucleic acid binding; IEA. GO; GO:0006309; P:DNA catabolism; IEA. InterPro; IPR008947; PLC Nuclease.
                                                                                                                                                                                                   298 AA.
                                                                                                        0; Mismatches
                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last seq 01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas putida (strain KT2440).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE=22423060; PubMed=12534463;
, AC002397, AAC36014.1; -., AK011313, BAB27539.1; -., AK001606. BAB25773.1; -., AK010409; BAB26316.1; -., AK028159; BAC25785.1; -.,
                                                                                                                                                                                                                                                      Senescence-associated protein 6
                                                                         Query Match
Best Local Similarity 100.0
States 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 ASESIS 240
                                                                                                                           1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASESIS 6
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=29711;
                                                                                                                                                                                                 081656
081656;
                               EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
Q88K39
                                                                                                                                                                                        à
                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
```

```
RAM MARIEON R.E., Mainel C., Paulsen I.T., Dedgen R.J., Hilbert H., RAM MARIEON R.E., Mainel C., Poulsen D.E., Gills E., Pop M., Hellnes M., Raineke L., Beather C., Beather M., Poulse D.E., Gills E., Pop M., Hellnes M., Raineke L., Beather M., Maine C., Beather M., Reine C., Reisen J., Timmis K.M., Duesterhoeft A., Themmler B., Rayles C., Elsen J., Timmis K.M., Duesterhoeft A., Themmler B., Rayles C., Elsen J., Timmis K.M., Duesterhoeft A., Themmler B., Rayles C., Elsen J., Timmis K.M., Duesterhoeft A., Themmler B., Rayles T., Maine M., Mapullane M., Mapullane M., Maine M
```

```
Tikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.",
Nat. Biotechnol. 21:526-531(2003).
EMBL, APONGOAT; BACTA235.1, "Complete genome sequence of a comparative analysis of the industrial language." Proceeding the process of the industrial net biotechnol. 21:526-531(2003).
InterPro, PRO03593; AAA_ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=2147403; PubMed=11572948;
MEDLINE=2147403; PubMed=11572948;
Millore M., Iskahashi Y., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horrikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M., "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 5; Length 483; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
Waterston R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO34759; AAP13762.1;
WormPep; Y37E11AR.7; CE33855.
InterPro; IPR007110; Ig-11ke.
Hypothetical protein.
SEQUENCE 483 AA; 55679 MW; AB174C4F622E3F46 CRC64;
                                                                                                                                                                           SEQUENCE FROM N.A.
STRAINED bristol N2;
Waterston R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                               Waterston R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                          Waterston R.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0828Y7;
01-UJN-2003 (TrEMBLrel. 24, Created)
01-UJN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative GTP-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metabolites.";
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 ASESIS 143
                                                              SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q828Y7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
Q828Y7
  REPRESENTATIONS OF SERVICE SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 100.0%; Score 25; DB 4; Length 449; Local Similarity 100.0%; Pred. No. 1.9e+02; es 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [3]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.H.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC047895; AAH47895.1;
InterPro; IPR000938; CAP-Gly.
Pfam; PF01302; CAP_GLY.
PROSITE; PS00845; CAP_GLY.
PROSITE; PS50245; CAP_GLY.2;
PROSITE; PS50245; CAP_GLY_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Miller N., Maggi L.;
"The sequence of C. elegans cosmid Y37E11AR.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    449 449 449 449 449 AA; 48881 MW; 2C46D1443E1438A8 CRC64;
                                    01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-UTN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
  449 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      483 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEJUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9651916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein Y37E11AR.7. Y37E11AR.7.
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 ASESIS 197
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [5]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
                                                                                                                                                                                                                                                                           rissum=Brain;
                     Q86WU4;
01-JUN-2003 (
01-JUN-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q86FM3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
```

ö

Gaps

.; 0

```
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                        U1-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 00)
                                                                                                    Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                  Prochlorococcus marinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                           Membrane GTPase LepA.
LEPA OR PRO0419.
                                                                                                                                                                         440 ASESIS 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544 ASESIS 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 6; Conserv
                                                                                                                                                    1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                             Q7VDF7;
                                                                                                                                                                                                                                  Q7VDF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7V2Q1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                           RESULT 13
Q7VDF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7V2Q1
  SERBERES
                                                                                                                                                    ò
                                                                                                                                                                         g
                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                              STRAIN-JCSC 4469;
MA X., Ito T., Okuna K., Hiramateu K.;
Ma X., Ito T., Okuna K., Hiramateu K.;
Mistorical distribution of SCCmec allotype in healthcare-associated
MRSA strains in Japan and Prance.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AB097677; BAC76058.1;
Hypotherical protein.
SEQUENCE 543 AA; 62077 MW; 9CD783183EBF075 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=DRN 1728;
MEDLINE=20479972;
PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                     / Match 100.0%; Score 25; DB 16; Length 491; Local Similarity 100.0%; Pred. No. 2.1e+02; nes 6; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 2; Length 543; 100.0%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermoplasma acidophilum.
Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                              491 AA; 53353 MW; 7BADD8E0449D14AC CRC64;
                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothetical membrane protein.
                                                                                                                                                                                                                                                                                                            Hypothetical protein. 24, Last annotation updat Hypothetical protein. Staphylococcus aureus. Bacteria, Firmicutes; Bacillales; Staphylococcus. NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                   543 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
 GTP-bindding_dom
           InterPro; IPR006073; GTP1_OBG.
InterPro; IPR002917; MMR HSR1.
InterPro; IPR005225; Small_GTP.
Pfam, PF01926; MMR HSR1, 1.
PRINTS; PR00326; GTP10BG.
SMRT; SM00382; AAA; 2.
TIGREAMS; TIGR00650; MG442; 2.
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
 InterPro; IPR005289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 ASESIS 418
                                                                                                     Complete proteome. SEQUENCE 491 AA;
                                                                                                                                                                                                        319 ASESIS 324
                                                                                                                                                                                  1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2303;
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                 Q83ZD8
Q83ZD8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9HJX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              оэнлх3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TA0839
                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
09HJX3
                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                       Q83ZD8
ò
                                                                                                                                                                                                        음
                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIR=SARG / CCMP 1375 / SS120;

MEDLINE=22810154; PubMed=12917486;

Dufresne A., Salanoubat M., Partensky F., Artiquenave F., Axmann I.M.,

Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,

Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,

Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,

Wolf Y.I., Hess W.R.,

"Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,

a nearly minimal oxyphototrophic genome.",

Proc. Natl. Acad. SCI. U.S.A. 100:10020-10025(2003).
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
MOBI_TaxID=59919;
                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae; Prochlorococcus.
                                                                                                                                                                                                                                      Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 16; Length 602; 100.0%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=22825698; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                 565 AA; 61966 MW; B78E9738C56A9B01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
SEQUENCE 602 AA; 67256 MW; 659E639EBF27D290 CRC64;
EMBL; AL445065; CAC11968.1; --
CO, CO.0004222; F:metalloendopeptidase activity; IEA.
CO; CO.0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR008915; Peptidase MO;
Pfam; PF02163; Peptidase MSO; 1.
CCMplete proteome.
SEGUENCE 565 AA; 61966 MW; B78E9738C56A9B01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
GTP-binding protein LepA.
LEPA OR PMM0420.
                                                                                                                                                                                                                                   100.0%; Score 25; DB 17;
100.0%; Pred. No. 2.4e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
```

us-09-635-974a-10.rspt

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22825698; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser B.R., Chisholm S.W.;
Webb E.A., Zinser B.R., Chisholm S.W.;
Nacure divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
Nature 424:1042-1047(203).
EMBL; BX572055, CAE20432.1; -.
Complete protecome.
SEQUENCE 604 AA; 67299 MW; FID561845D76A804 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M., Shaw S.L., Sreglich C., Sullivan M.B., Ting C.S., Tolonen A., Webb E.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation.";
Nature 424:1042-1047(2003).
EMBL: BXSTOSO1, CAB18879.1; -.
Complete protecome.
SEQÜENCE 602 AA; 67457 MW; 5916A6E964658E90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcase; Prochlorococcus.
NCBL_TaxID=74547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 16; Length 604; 100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                          h 100.0%; Score 25; DB 16; Length 602; Similarity 100.0%; Pred. No. 2.6e+02; 6; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7V854;
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
GTP-binding protein LepA.
LEPA OR PMT0257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 604 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: October 6, 2004, 16:34:02 Job time: 25.1053 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544 ASESIS 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       544 ASESIS 549
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ASESIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7V8S4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
OV884
OV884
OCTV88
AC 07088
AC 0708
DT 01-0C
DT
                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

Q84fl0 pantoea agg Q8t8nd caenorhabdi Q9p3n7 neurospora P91350 caenorhabdi Q26812 methanobact Q9129 citrus yell Q9xym9 trichomonas Q9ty183 homo sapien Q8kqp3 anaplasma p Q8kqp2 anaplasma p Q8kqq2 anaplasma p Q8tp6 anaplasma p Q8

084FL0 0818M4 0818M4 0818M4 026812 021812 021812 031M13 037M13 037M2 038R2 038R2 038R2 038R2 038R2 038R2 038R2 038R2 037R0 037R0 037R0 061611 06101

```
October 6, 2004, 16:23:13 ; Search time 30.1579 Seconds (without alignments) 94.160 Million cell updates/sec
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                  1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                      sp_bacteria:*
sp_bacteria:*
sp_human:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
sp_organelle:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_plant:*
sp_pordant:*
sp_vorebrate:*
sp_vorebrate:*
sp_vorebrate:*
sp_vorebrate:*
sp_vorebrate:*
sp_vorebrate:*
sp_vorebrate:*
sp_vorebrate:*
                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                           US-09-635-974A-12
56
1 QQNNNWPTT 9
                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                 SPTREMBL
                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                    Scoring table:
                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                 Database
                                                                   Run on:
```

084967 Q7VN12 Q885P1 Q814G9

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 2 QBR011

| •                               | te) iila). iickettsiales; phagocytophila msp2 CRC64;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | gth 160;<br>Indels 0; Gaps                                        |            |
|---------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|------------|
| 160 AA.                         | 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annocation update) 01-MAR-2003 (TrEMBLrel. 23, Last annocation update) Major surface protein hypervariable region (Fragment) MSP2. MAPAplasma phagocytophilum (Ehrlichia phagocytophila). Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales Anaplasmataceae; Anaplasma. Anaplasmataceae; Anaplasma. MOTILTAXID=948; 101 SERQUENCE FROM N.A. SERQUENCE FROM N.A. MEDLINE=21843110; PubMed=11854205; Gaspersen K., Park J.H., Patil S., Dumler J.S.; Gaspersen K., Park J.H., Patil S., Dumler J.S.; Menetic variability and stability of Anaplasma phagocytophi. Infect. Immun. 70:1230-1234 (2002). EMBL; AF443406; AAL9174.1; EMBL; AF443406; AAL9174.1; Effect. Immun. 70:1230-1234 (2002).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 2; Len<br>2;                                                      |            |
| PRT;                            | rel. 21, Created) rel. 23, Last sequence of Last sequence of Last annotation of Last sequence of Last sequen | 71.4%; Score 40; DB<br>75.0%; Pred. No. 30;<br>iive 0; Mismatches |            |
| PRELIMINARY;                    | 01-UUN-2002 (TrEMBLrel. 21, Created) 01-UUN-2002 (TrEMBLrel. 21, Last sequ M10-2002 (TrEMBLrel. 21, Last sequ 01-MAR-2003 (TrEMBLrel. 23, Last anno Major surface protein hypervariable rang MSP2. Anaplasma phagocytophilum (Ehrlichia Bacteria; Proteobacteria; Alphaproteo Anaplasmataceae; Anaplasma. NCBI_TAXID=948; [1] [1] [2] [2] [2] [3] [3] [4] [4] [4] [5] [5] [6] [6] [6] [6] [7] [7] [7] [7] [8] [8] [8] [8] [8] [8] [9] [9] [9] [9] [9] [9] [9] [9] [9] [9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | , va                                                              | OONNWWPT 8 |
| RESULT 1<br>QBRP67<br>ID QBRP67 | Ol-JUN-2002 (TERME OI-JUN-2002 (TERME OI-JUN-2003 (TERME) (TERME OI-JUN-2003 (TERME) ( | Query Match<br>Best Local Similarity<br>Matches 6; Conser         | <b>-</b>   |

```
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       2 QNNNWPT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QNINIWPT 8
SEQUENCE FROM N.A.
                Inoue J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ab2-389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9AAL8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
Q9AAL8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7TP45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAHAHA
 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SERAIN=C57BL/G-1 IISSUB=Thymus;
MEDIAINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
Wommalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for high-rate new gene discovery.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Thymus;
Adachi J., Alzawa K., Akimurs;
Adachi J., Alzawa K., Akimurs T., Arakawa T., Bono H., Carninci P.,
Adachi J., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kanamori M.,
Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H.,
Nakamura M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M.,
Nakamura M., Nishi K., Nomura K., Numasaki R., Ohno M., Ohsato N.,
Okazaki Y., Sasitoh H., Sakai K., Sakazume N.,
Sano H., Sasaki D., Shibata K., Shihnagawa A., Shiraki T., Sogabe Y.,
Suzuki H., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S.,
Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/61; TISSUE-Thymus;

MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watsumagi K., Fujiwake S., Inoue K., Tozawa K., Tanaka T., Matsuura S., Kawai J., Rohazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rikis integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kanamori M., Suzuki H., Salto R., Muramatsu M., Hayashizaki Y., "T2BP, a Novel TRAR's Binding Protein, Can Activate NF-kB and AP-1 without TNF Stimulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                           01-070-2002 (TrEMBLrel. 21, Created)
01-070-2002 (TrEMBLrel. 21, Last sequence update)
01-070-2003 (TrEMBLrel. 25, Last annotation update)
TRAF2 binding protein (TIFA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 290:1108-1113(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINB=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21656991; PubMed=11798190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [6]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID=10090;
                Q8R011;
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CS/BL/60; TISSUE=Retina;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
MANALYSIS of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.

Xu C.S., Li W.Q., Li Y.C., Wang G.P., Chai L.Q., Yuan J.Y., Yang K.J.,
Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F., Han H.P.,
Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
"Liver regeneration after PH.",
"Liver regeneration after PH.",
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY325204; AAP92605.1;
EEMBL, AAP3605.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.4%; Score 40; DB 11; Length 184; 85.7%; Pred. No. 35; 1; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 11; Length 421; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                          EMBL; AKO41891; BAB86846.1; -.
EMBL; AKO4121; BAB86903.1; -.
EMBL; AB06211; BAB86903.1; -.
EMBL; AM04221; BAC31825.1; -.
MGD; MG1:218265; T2bp.
GO; GO:0007249; PINK-Ir-kappaB/NF-kappaB cascade; IDA.
GO; GO:0007249; PINK-Ir-kappaB/NF-kappaB cascade; IDA.
InterPro; IPR008984; SMAD_FHA.
SMRAT; SM0240; FHA.
PROSITE; PSSGO066; FHA.
PROSITE; PSSGO066; FHA.
SRQUENCE 184 AA; 21560 MW; 1466F2A7307F03E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
"TIFA, a novel TRAF6 binding protein.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7TP45 PRELIMINARY; PKI; 441 MA. Q7TP45; 01-OCT-2003 (TrEMBLrel. 25, Created) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09AAL8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
TonB-dependent receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                972 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.4%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 QENNWPT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 QENNWPT 397
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VTB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
Q9VTB8
         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    심
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCOORDITATION OF THE SECTION OF THE
                                               REQUENCE FROM N.A.

REATN=ATC 19089 / CB15;

RA MEDLINE=21173699; PubMed=11259647;

RA MEDLINE=21173699; PubMed=11259647;

RA Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RA Bero J., Heidelberg J.F., Alley M.R.K., Ohra N., Maddock J.R.,

RA Deboy R.T., Dodson R.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA Deboy R.T., Durkin A.S., Gwinn M.L., Haft D.H.,

RA Congy J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

RT "Complete genome sequence of Caulobacter crescentus.";

RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

BREMEL, ABC005732; AAK22565.1; -.

REMEL, ARCOS732; AAK22565.1; -.

REMEL, ARCOS732; AAK22565.1; -.

REMEL, ARCOS732; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=KIMS / Blovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
Deng W. Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21470413; PubMed=11586360; Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prarkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamiln N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Jagels K., Karlyshev A.V., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Genome sequence of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Versinia pestis.
Bateriai, Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriacae, Yersinia.
VCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.4%; Score 40; DB 16; Length 972; 75.0%; Pred. No. 1.9e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         972 AA; 104732 MW; B599CDD10C26AC4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Putative membrane protein (Putative sulfatase)
YPO1260 OR Y2924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      598 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000531; TonB boxC. Pfam; PF00593; TonB dep Rec; I. Receptor; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                               Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 ENPNWPIT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 QNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8ZGM7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8ZGM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8ZGM7
δ
```

```
REPUBLINE=SUDBANCE FROM N.A.

REDINE=SUDBANCE FROM N.A.

REDINE=SUDBANCE FROM N.A.

REDINE=SUDBANCE FROM N.A.

RA Amanatides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Change M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej K.G., Change M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., Baxman B.P., Bhandari D., Bolshakov S.,

RA Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Bolckstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Downes M., Digan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.B., Downes M., Digan-Rocha S., Dunkov B.C., Dunn P.,

RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Hostin D., Houston K.A., Howland T.J., Wei M. Harris M.,

RA Hostin D., Houston K.A., Howland T.J., Wei M. H., Ind Y., Mattel B., McIncosh T.C., McLed M., Moherson D.,

RA Liu X., Mattel B., McIncosh T.C., McLedd M.D., Mohriscon D.,

RA Mount S.M., Moy M. Murphy B., Murphy L., Murzhy D., Puri V., Palazolo M., Palesce McGallard J., Palazolo M., Palazolo M., Palesce McGallard J., Palazolo M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota; Neoptera; Endotterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                      PIR; ACUISA; ACUISA;

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0008481; F:receptor activity; IEA.

R GO; GO:0008481; F:sulfuic ester hydrolase activity; IEA.

R GO; GO:0008215; F:sulfuic ester hydrolase activity; IEA.

R GO; GO:0008152; F:ransporter activity; IEA.

R GO; GO:0008152; P:metabolism; IEA.

R GO; GO:0008152; P:metabolism; IEA.

R InterPro; IPR000531; TonB_boxC.

R InterPro; IPR000531; TonB_boxC.

R PROSITE; PS00430; TONB_DEPENDENT REC_1; 1.

W HYPOCHAELICAL profesin; Complete proceome.

SEQUENCE 598 AA; 67474 MW; CGEE2A0BDCIE43A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 16; Length 598;
Pred. No. 2.5e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.1-MX-2000 (TrEMBLrel. 13, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
CG7958 protein (LD16921p).
TNA OR CG7958.
"Genome sequence of Yersinia pestis KIM."; Datterio1. 184:4601-4611(2002).
EMBL; AJ414147; CAC90094.1; -.
EMBL; AS013894; AAM86475.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 66.7
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 QRNNNWVAT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QQNNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
```

ö

```
α
                                       RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                    28V3P6
                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                  Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A McIntosh T.C., May M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
A Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drossophila melanogaster genome.",
L. Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Spiue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Zheng X.H., Zhong F.N., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith B., Shu S., Smurniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
"Annotation of Drosophila melanogaster genome.",
submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=y; Sapayani A., Carlson J., Sapayani A., Carlson J., Sapayani A., Carlson J., Sapayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mingall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.B., Rubin G.M., Celniker S.; Naconstanted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BT003272; AA025029.1; --
FlyBase; FEGIN03613; tha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 5; Length 1109; Pred. No. 4.7e+02; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1109 AA; 116491 MW; 4FD726183EE642AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0008270; F:zinc ion binding; IEA.
InterPro; IPR004181; Znf MIZ.
Pfam; PF02891; zf-MIZ; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPROC
Pfam; PF02891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :lyBase;
                SORRER PRESENTED TO SERVICE SE
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22144240; PubMed=12149362;

Lin Q., Zhi N., Ohashi N., Horowitz H.W., Aguero-Rosenfeld M.E.,

Lin Q., Zhi N., Wormer G.P., Rikihisa Y.,

"Analysis of Sequences and Loci of p44 Homologs Expressed by Anaplasma

phagocytophila in Acutely Infected Patients.";

Clin. Microbiol. 40:2981-2988 (2002).

EMBL, Ay064519; AAL78182.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                 STRAIN=17077-99;
MEDLINE=21624277; PubMed=11752168;
Afonso C.L., Tulman B.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
Kutish G.F., Rock D.L.;
"The genome of swinepox virus.";
J. Virol. 76:783-790(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                            Afonce C.L., Tulman E.R., Lu Z., Balinsky C., Osorio F.A., Zsak L., Rutish G.F., Rock D.L.;
Rutish G.F., Rock D.L.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF410153; AAL69787.1; -.
GO; GO:0016020; C:membrane; I.E.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:007156; P:homophilic cell adhesion; IEA.
InterPro; IPR002156; Cadherin.
Hypothetical protein.
SEQUENCE 111 AA; 13043 MW; AF715FFF23E704EB CRC64;
                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P44-30.
Anaplasma phagocytophilum (Ehrlichia phagocytophila).
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 12; Length 111; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13416 MW; 6F735572B031DFD1 CRC64;
                  Q8V3P6;
01-MAR-2002 (TrEMBLrel. 20, Created)
MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
SPV049 hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
44 kDa major outer membrane protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 2;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 AA.
111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.1%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.1%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anaplasmataceae; Anaplasma.
NCBI_TaxID=948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 QONNIPT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 130 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QONNNWPT 8
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=10276;
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=17077-99
                                                                                                                                        Swinepox virus.
                                                                                                                                                                                Suipoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8KQQ0
Q8V3P6
```

Best Local Similarity

.; 0

Gaps

.

0; Mismatches

6; Conservative

Matches

à

**083VVS** 

```
STRAIN=EI TOT N16961 / Serotype O1;
STRAIN=EI TOT N16961 / Serotype O1;
MEDLINE=204068313; PubMed=10952301;
Heidelberg J.F., Bienen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-22170783; PubMed=12183586;
IJdo J.W., Wu C., Telford S.R., Pikrig E.;
"Differential expression of the p44 gene family in the agent of human
granulocytic ehrlichiosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anaplasma phagocytophilum (Ehrlichia phagocytophila).
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Anaplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 16; Length 153;
Pred. No. 91;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ijdo J.W.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF512671; AAP14021.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; VC1803; -- Hypothetical proteome.

SEQUENCE 153 AA; 17480 WW; C92B7B307501A722 CRC64;
                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        084106;
01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence updat
01-UTN-2003 (TrEMBLrel. 24, Last annotation upd
Major outer membrane protein SC1-1 (Fragment)
                                                                                                                                                                                                                                                           153 A.A.
                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nfect. Immun. 70:5295-5298(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).
EMBL; AE004257; AAF94952.1; -.
PIR; H82153; H82153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.1%;
62.5%;
                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24, Hypothetical protein VC1803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |:||||
65 EENSWPTT 72
                                                                            |:||||:
89 NHWWPTS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ONNWWPIT 9
                                    3 NNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cholerae.
                                                                                                                                                                                                                                                    Q9KR43
Q9KR43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 084106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                    ò
                                                                                  g
                                                                                                                                                                                                                                                                                     ACCOOR SERVING                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barbet A.F., Meeus P.F.M., Belanger M., Bowie M.V., Yi J., Lundgren A.M., Alleman A.R., Wong S.J., Chu F.K., Munderloh U.G., Jauron S.D.;
"Expression of multiple outer membrane protein sequence variants from a single genomic locus of Anaplasma phagocytophilum.";
Infect. Immun. 71:1706-118 (2003).
EMBL, AX164497; AA0301091.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jauron S.D.;
"Expression of multiple outer membrane protein sequence variants from a single genomic locus of Anaplasma phagocytophilum.";
Infect. Immun. 71:1706-1718(2003).
EMBL; AY164505; AAO30117.1; -.
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barbet A.F., Meeus P.F.M., Belanger M., Bowie M.V., Yi J.,
Lundgren A.M., Alleman A.R., Wong S.J., Chu F.K., Munderloh U.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anaplasma phagocytophilum (Ehrlichia phagocytophila).
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Major surface protein 2 (Fragment)
Major surface protein 2 (Fragment)
Daplasma phagocytophilum (Ehrlichia phagocytophila).
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.1%; Score 37; DB 2; Length 134; 71.4%; Pred. No. 80; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 66.1%; Score 37; DB 2; Length 139; Best Local Similarity 71.4%; Pred, No. 83; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 134
134 AA; 13573 MW; 67E791D5303C15B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139
14576 MW; 6C96C03CC55E121A CRC64;
                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Major surface protein 2 (Fragment)
   .;
                                                                                                                                                                                                                                                                                     134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 AA
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=var B;
MEDLINE=22541496; PubMed=12654783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=var A;
MEDLINE=22541496; PubMed=12654783;
   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anaplasmataceae; Anaplasma.
NCBI_TaxID=948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anaplasmataceae; Anaplasma.
NCBI_TaxID=948;
Conservative
                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 13
139 AA;
                                                           ONNWWPT 8
                                                                                                                          81 ENKNWPT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENKNWPT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 QNNNWPT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
NON TER
SEQUENCE
                                                           N
```

NON TER

Best Loc Matches

g

Q83VU7 RESULT 10 Q83VU7

ö

Gaps

ô

```
|||:|||
280 NNNYPTT 286
                                                                                                                                                                                                                                                                                                                                                                                   1 QONNNWPT 8
                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 452 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Job time : 34.1579 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8F9N5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8F9N5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
Q8F9NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC OC OC SERVER TO SERVER SERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.; "The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=HZ;
MEDLINB=21843103; PubMed=11854198;
SIN N., Ohashi N., Tajima T., Mott J., Stich R.W., Grover D.,
Telford S.R. III, in Q., Rikhinsa Y.;
"Transcript heterogeneity of the p44 multigene family in a human
granulocytic christniosis agent transmitted by ticks.";
                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI TaxID=28227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anaplasma phagocytophilum (Ehrlichia phagocytophila).
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Anaplasma.
NCBI_TaxID=948;
                                                                                      Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                      166 166
166 AA; 17205 MW; 6997EFAD6D745C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 178 178 178 178 AA; D05889A564A848F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Major outer membrane protein P44-16 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.1%; Score 37; DB 2; I
71.4%; Pred. No. 1.1e+02;
tive 1; Mismatches 1;
                                                                                 Query Match
Best Local Similarity 71.4%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                            178 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                452 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22354719; PubMed=12466555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP004170; BAC43791.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma penetrans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 ENKNWPT 108
                                                                                                                                                                                                                  101 ENKNWPT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 QNNNWPT 8
                                                                                                                                                                       2 QNNNWPT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=HF-2;
NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8EX49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYPELO
                                                                                                                                                                                                                                                                                                                          QBRPC0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.1%; Score 37; DB 16; Length 452; Best Local Similarity 62.5%; Pred. No. 2.8e+02; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 503;
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003689; F:DNA replication origin binding; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0006275; P:Nucleotide binding; IEA.
GO; GO:0006275; P:regulation of DNA replication; IEA.
InterPro; IPR00359; Para ATPase.
InterPro; IPR00359; Bac_DnaA.
Pfam; PF00308; bac dnaA; 1.
PRINTS: RR00051; DNAA.
SNART; SM0082; AAA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren S.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AE011207; AAW47355.1;
Hypothetical protein; Complete proteome.
SEQUENCE 503 AA; 57820 MW; C50EFFADC2366792 CRC64;
                                                                                                                                                                                                                                                                                                                         452 AA; 52977 MW; A853FC934F25F0E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.1%; Score 37; DB 16;
85.7%; Pred. No. 3.1e+02;
ative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: October 6, 2004, 16:34:06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last seq 01-MAR-2003 (TrEMBLrel. 23, Last ann Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 85.7
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 EENNNWKT 144
```

```
MEDLINE=77038198; PubMed=824717;

REDLINE=77038198; PubMed=824717;

REDLINE=77038198; PubMed=824717;

REDLINE=77038198; PubMed=824717;

REDLINE=7704 and Sequence of the variable domains of two human gradulous and sequence of the variable domains of two human gradulous and sequence of the variable domains of two human gradulous and sequence of the variable dottypic

REDLINEST TEMPERS TOWN THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ANTH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINATS.

CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINATS.

CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, STANDARD THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

RESP. PO1667; IREI

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005955; P:immune response; NAS.

RICEPERO; IPRO07110; Ig-11ke.

RESP. PRO07110; Ig-11ke.
              Q12659 pentatung
P09849 orycrolagus
O27471 homo sapien
O23676 arabidopsis
O9m2K6 macaca mula
P24017 klebaiella
P21613 drosophila
P20034 escherichia
P2775 serraria ma
P2441 arbacia lix
O51402 borrelia bu
    ruminococcu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 75.0%; Score 42; DB 1; Length 108; Local Similarity 77.8%; Pred. No. 1.7; es 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108
11834 MW; 739993A95431434A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
16 kappa (Alain V-I region Lay.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK-1
                ARO1_PNECA
PLAB HABIT
PLAB HUMAN
MGN ARATH
NKGC MACMU
OMPA KLEPN
PER DROIN
THRC ECOLI
THRC SERNA
NUAM ARBLI
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF00047; ig; 1.
SMART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
954
1926
1158
1150
1150
1231
3344
428
429
586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
34
49
56
88
97
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QOYNVWPPT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O LIAMNINIOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
35
50
57
89
98
108
KV1M HUMAN P01605;
  Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                           KV1M_HUMAN
                                                                                                                                                                                                                                                                                                                                        RESULT 1
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homo sapien
homo sapien
homo sapien
agaricus bi
bacillus su
schizosacch
mus musculu
rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  c genome po
c genome po
e genome po
pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mus musculu
chloris str
pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xylella fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               buchnera ap
cryphonectr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xylella fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chlamydia t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                 ; Search time 5.52632 Seconds (without alignments) 84.800 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P01665
P0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9cky6
P36202
Q8k9a7
Q00548
P77779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P43666
P44779
O97297
P16109
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                           141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PASMU
MOUSE
CSMV
PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGABI
BACSU
SCHPO
MOUSE
RAT
MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHLTR
ECOLI
CAEEL
CXB4E
CXB4E
CXB5P
EC30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BUCAP
CRYPA
ECOLI
MYCGA
                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAEIN
SULSO
HUMAN
                                                                                                                                     6, 2004, 16:21:13
                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RADC.
                                                                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 2000000000
                                                                                                                                                                                                               US-09-635-974A-12
56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SwissProt_42:*
                                                                                                                                                                                                                                                        QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221178
211883
11094
11094
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
11024
1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            591
                                                                                                                                       October
                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                       score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                               Title:
Perfect s
                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
No.
```

ö

```
EMBL; M12740; AAA58992.1; -. HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 QQYNNWP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QONNNWP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=D649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CELL AGABI
Q00023;
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEL1_AGABI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                          MEDLINE=76276460; PubMed=60899;
Klapper D.G., Capra J.D.;
Klapper D.G., Capra J.D.;
"The amino acid sequence of the variable regions of the light chains from two idiotypically cross reactive IgM anti-gamma globulins.";
Ann. Immunol. (Paris) 127C:261-271(1976).
-! MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
PIR; A01897; K3HUPM.
HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=86177570; PubMed=3083417;
Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
Goldien R., Carson D.A.;
Glohing and sequence determination of a human rheumatoid factor
light-chain gene.";
Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
                                                                                                                                                                              Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1987 (Rel. 04, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region CLL precursor (Rheumatoid factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%; Score 42; DB 1; Length 109; 77.8%; Pred. No. 1.7; 2; Indels iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;
                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1G kappa chain V-III region POM.
                                          109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, PR0362, IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955: P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF00047, ig; 1.
SMART, SMO4066, IGv. 1.
PROSITE, PS50835, IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 OVNINWPPT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QONNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KV3H_HUMAN
P04207;
                                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                            KV3F HI
P01624
                                               DDARKER REPRESENT OF THE PROPERTY OF THE PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITIRE 9427428; PubMed=8181702;
Armesilla A.L., Thurston C.F., Yaguee E.;
Armesilla A.L., Thurston C.F., Yaguee E.;
Armesilla A.L., Thurston C.F., Yaguee E.;
bisports during growth on crystalline cellulose.";
FEMS Microbiol. Lett. 116:293-299(1994).
-:- FUNCTION: PROBABLE GLYCOSYL HYDROLASE ACTIVE ON CELLULOSE..
-:- SUBCELLULAR LOCATION: Secreted..
-:- SUBCELLULAR: CONTION: Secreted..
-:- SIMILARITY: Contains I fungal-type cellulose-binding (CBD) domain..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=D649;
MEDLINE=93012985; PubMed=1398098;
Raguz S., Yaguee E., Wood D.A., Thurston C.F.;
"Isolation and characterization of a cellulose-growth-specific gene from Agaricus bisporus.";
Gene 119:183-190(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agaricus bisporus (Common mushroom).
Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Homobasidiomycetes,
Agaricales, Agaricaceae; Agaricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                          IG KAPPA CHAIN V-III REGION CLL. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 1; Length 129; Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14275 MW; 5C13B411BE60CC14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cellulose-growth-specific protein precursor CEL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 9.1;
0; Mismatches
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobuliv region; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.9%;
85.7%;
```

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cyclase)
      SOW SOW SOUTH STREET ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINES POYAUS; FUDGUESCOSS, //
A KURST F., OGASGWART N., MORGER I., Albertini A.M., Alloni G.,
A Zevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Borriss R., Boursier L., Brans A., Bran M., Brighell S.C., Bron S.,
Brouillet S., Bruschi C.V. Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
A Denizot F., Devine K.M., Dusterhôft A., Ehrlich S.D., Emmerson P.T.,
Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Britan K.D., Errington J., Pabret C., Perrari E., Foulger D.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Laylus A., Lardinols S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                            HSSP, P00725; 2CBH.
InterPro; PR000254; CBD fungal.
InterPro; IPR000254; CBD fungal.
Pfam; PF00734; CBM 1; 1.
Pfam; PF00734; CBM 1; 1.
Pfam; PF00734; Glyco_hydro_61; 1.
Pfam; PF00516; fCBD; 1.
PROSITE; PS0056; CBD FUNGAL; 1.
Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EC 5.3.1.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=168 / Marburg;
MEDLINE=96349105; PubMed=8760912;
Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                     CELLUIOSE-GROWTH-SPECIFIC PROTEIN.
CATALYTIC (POTENTIAL).
LINKER (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60E2C8080895CA2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase
keto-4-deoxyuronate isomerase) (DKI isomerase).
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
   entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33754 MW;
                                                                                      EMBL; M86356; AAA53434.1; -. PIR; JC1311; JC1311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 75.0
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 QNNSWTTT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 QNNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303
163
320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1423,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (
01-OCT-1996 (
10-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDUI BACSU
P50843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
KDUI_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCOORDINATION OF THE STATE OF
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWIS, outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Medina N., Mellado R.P., Miruno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pobl T.M., Portetalle D., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
A Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sektouchi J., Skowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Mambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Roshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
subtilis "."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
MEDLINE=89345533; PubMed=2668944;
Yamawaki-Kataoka Y., Tamaoki T., Choe H.-R., Tanaka H., Kataoka T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALWIIC ACTIVITY: 4-deoxy-L-threo-5-hexosulose uronate = 3-deoxy-D-glycero-2,5-hexodiulosonate.
-!- PATHWAY: Pectin degradation.
-!- SIMILARITY: Belongs to the kduI family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEQUENCE FROM N.A.
MEDLINE=90046723; PubMed=2682634;
Young D., Riggs M., Field J., Vojtek A., Broek D., Wigler M.;
"The adenylyl cyclase gene from Schizosaccharcmyces pombe.";
Proc. Natl. Acad. Sci. U.S.A. 86:7989-7993(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isomerase; Complete proteome.
SEQUENCE 275 AA; 31135 MW; 31B2CE2CE7C54760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 1;
Pred. No. 29;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L47838; AAB38477.1; -.
EMBL; Z99115; CAB14130.1; -.
PIR; E69648; E69648;
Subtilist; BG11401; kduI.
HAMAP; MF 00687; -; 1.
InterPro; TPR007045; KduI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.,
دم 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF04962; KduI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 QNNNWNT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYR1 OR SPBC19C7.03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 QNINNWPT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYAA SCHPO
P14605;
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=81220975; PubMed=6264318;
MEDLINE=81220975; PubMed=6264318;
MEDLINE=81220975; PubMed=6264318;
Mechanis Maline and rearranged immunoglobulin V kappa coding sequences between germ-line and rearranged immunoglobulin V kappa natherences between germ-line and rearranged immunoglobulin V kappa coding sequences suggest a localized mutation mechanism.";
Nature 291:668-670(1981).
-I- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICE JUNCTIONS AT THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN LACKING RESIDUES 17-19.
       PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS50200; RA; 1.
Lysne: Psecat; Leucine-rich repeat; cAMP blosynthesis; Metal-binding; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                    Length 1692;
                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1; Length 169
Pred. No. 1.8e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                          MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
W; D137CBE8770A8655 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATE MOUSE STANDARD, PRT, 115 AA. 121-142, 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 19 kappa chain V-V region L7 precursor (Fragment).
                                                RAS-ASSOCIATING.
LRR 1.
                                                                                                                                                                                                                                                                                                                                 1692 AA; 190333 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR, A01925; KVMSL7.
PDB; 1J10; 18-FEB-03.
PDB; 1J1X; 18-FEB-03.
INTERPRO; 1PR007110; 1g-like.
INTERPRO; 1PR003596; 1g_v.
Ffam; PF00047; ig; 1.
SMART; SM00406; igv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                    66.1%;
                                                                                                                                                                                                                                                                                                                                                                71.4%;
                                                                                                                                                                                                                                                                                                                                                                Local Similarity 71.4
nes 5; Conservative
SM00314; RA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                    198 NNNWPAS 204
                                                                                                                                                                                                                                                                                                                                                                                              3 NNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                    DOMAIN
                                                                      REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                         REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KV51_MOUSE
                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
à
```

```
CEF397A066BF0986 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; I
5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                            (GLONAC.
(GLONAC.
(GLONAC.
(GLONAC.
(GLONAC.
(GLONAC.
(GLONAC.
(GLONAC.
(GLONAC.
(GLONAC.
(GLONAC.
(GLONAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36;
Pred. No.
 CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2875
2894
2939
2979
1, 365448 N
  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                           1016
1169
1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      855
816
855
855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2048
2127
2166
2193
2261
2355
2367
                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYL
                                                                                                                                           DOMAIN
                                                                                                                                                                           DOMAIN
   DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                           DOMAIN
                                                                                                           DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                 DOMAIN
                                                                  DOMAIN
                                                                                                  DOMAIN
                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                             DOMAIN
  SIMILARITY:

SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

This SWISS-RROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprehensive analysis of large CDNAB.";
Brain Res. Mol. Brain Res. 94:85-95(2001).
-!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
- They preferentially interact with themselves in a homophilic manner in connecting cells. Cadherin 23 may function as hair bundle organizer perhaps by cross-linking the stereocilia (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB053447; BAB61904.1; -.
InterPro; I PR000216; Cadherin.
PFEM; PR000208; CADHERIN.
PRINTS; PR00129; CADHERIN.
SMART; SM00112; CA. 26.
PROSITE; PS00232; CADHERIN 1; 17.
PROSITE; PS0028; CADHERIN 1; 17.
Call adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat; Signal; Multigene family.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Sprague-Dawley, TISSUE-restis,
BEDLINES-1481446; PubMed-11597768;
Nakajima D., Nakayama M., Kikuno R., Hirosawa M., Nagase T., Ohara (
"Identification of three novel non-classical cadherin genes through
                                                                                                                                                                 ·.
                    IG KAPPA CHAIN V-V REGION L7.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                          FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.
                                                                                                                                         64.3%; Score 36; DB 1; Length 115; llarity 71.4%; Pred. No. 17; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CADHERIN-23.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                      C17BEC758C577E00 CRC64;
 Signal; 3D-structure.
                                                                                                                                                                                                                                        CADN_RAT

1D CADN_RAT

1D CABON_RAT

1D CABON_RAT

1D CABON_RAT

1D CABON_RAT

1D CABON_RAT

1D 28-FEB-2003 (Rel. 41, Created)

1D 28-FEB-2003 (Rel. 41, Last sequence update)

1D 10-CTT-2003 (Rel. 42, Last annotation update)

1D CABORIN-23 precursor (Otocadherin).
                                                                                                                       12615 MW;
  V region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
3317
3062
3083
3317
                                                                                                                                                                                                  109 QQSNSWP 115
                                                                                                                       AA;
                                                                                                                                                    Similarity
5; Conserv
                                                                                                                                                                                     1 QQNNNWP 7
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                           115
115 A
Immunoglobulin
SIGNAL
                    CHAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DISULFID
NON TER
SEQÜENCE
                                                                                                                                           Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
DOMAIN
TRANSMEM
DOMAIN
  STITETTE
                                                                                                                                                                                      ò
                                                                                                                                                                                                           유
```

(POTENTIAL)

(POTENTIAL) (POTENTIAL) (POTENTIAL) POTENTIAL)

(POTENTIAL)

Length 3317;

us-09-635-974a-12.rsp

```
---
÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawai J., Shinagawa M., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A. Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Osyazaki Y., Gojobori T., Bono H., Ksukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F., Blake J., Bolt C., Fletcher C., Fujita M., Gariboldi M., Abroms P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitteker C., Wliming L., Washing K.H., Weitz C., Whitteker C., Wliming L., Warshii J., Kawaji H., Kohtsuki S., Lyons P., Wonsha-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21280917; PubMed=11386759; Wilson S.M., Householder D.B., Coppola V., Tessarollo L., Fritzsch B., Lee E.-C., Goss D., Carlson G.A., Copeland N.G., Jenkins N.A.; ""Mutations in Cdh23 cause nonsyndromic hearing loss in waltzer mice."; Genomics 74:228-233 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [5]
GENOMIC ORGANIZATION, ALTERNATIVE SPLICING, VARIANT WALZER
GENOMIC ORGANIZATION, ALTERNATIVE SPLICING, VARI-229; LYS-881;
LLB-1137; ARG-1236; VAL-2025; VAL-2026; THR-2217; HIS-2222; ARG-2270
AND ALA-2617.
MEDLINE-21623040; PubMed=11750125;
Di Palma F., Pellegrino R., Noben-Trauth K.;
 Gaps
                                                                                                                                                                                                                                                                                                                       Belyantseva I.A., Pellegrino R.,
                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                     Di Palma F., Holme R.H., Bryda E.C., Belyantseva I.A., Pellegrino Kachar B., Steel K.P., Noben-Trauth K.; "Mutations in Cdh23, energa a new type of cadherin, cause stereocilia disorganization in waltzer, the mouse model for Usher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annotation of a full-length mouse cDNA collection.";
ô
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Fu Y., Wang Q., Roe B.A.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 .
0
                                                                                                                                                           Last sequence update)
Last annotation update)
 Mismatches
                                                                                                                                                                                       (Otocadherin)
                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J;
MEDLINE=20578758; PubMed=11138008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                099PP4, 099NH1, 09D4N9,
28-FBB-2003 (Rel. 41, Last seq.
28-FBB-2003 (Rel. 41, Last seq.
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                           syndrome type 1D.";
Nat. Genet. 27:103-107(2001).
 5; Conservative
                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001)
                                                                                                                                                                                      Cadherin-23 precursor
                                                 2061 NDNWPT 2066
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                         3 NNNWPT 8
                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Functional
                                                                                                                     CADN MOUSE
 Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       Isola 2099PF4-2; Sequence-VSP 000648;
Isosus SPECIFICITY: In adult animals relatively high levels of expression are found in testis, skeletal muscle, heart, eye and thymus, and lower expression in kidney, lung and brain. Found in the sensory hair cells of the inner ear.

NalsaAss Defects in CDH23 are the cause of waltzer (v) phenotype. Waltzer mice are characterized by deafness and vestibular dysfunction due to degeneration of the neuroepithelium within the
"Genomic structure, alternative splice forms and normal and mutant alleles of cadherin 23 (Cdh23).";
Gene 281:31.41(2001).
-!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
They preferentially interact with themselves in a homophilic manner in connecting cells. Cadherin 23 may function as hair bundle organizer perhaps by cross-linking the stereocilia.
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- ALTERNATIVE PRODUCTS:
EVent-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat; Signal; Multigene family; Alternative splicing; Deafness; Polymorphism; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CADHERIN-23. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTENIAL.
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
CADHERIN 7.
CADHERIN 9.
CADHERIN 11.
CADHERIN 11.
CADHERIN 11.
CADHERIN 12.
CADHERIN 13.
CADHERIN 14.
CADHERIN 14.
CADHERIN 15.
CADHERIN 15.
CADHERIN 16.
CADHERIN 16.
CADHERIN 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 27 cadherin domains
                                                                                                                                                                                                                                                                                                                                     IsoId=099PF4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF308939, AAG52817.1; -.
EMBL, AV026062; AAK07670.1; -.
EMBL, AK016365; -; NOT_ANNOTATED_CDS.
EMBL, AC079818; -; NOT_ANNOTATED_CDS.
EMBL, AC079819; -; NOT_ANNOTATED_CDS.
EMBL, AC079819; -; NOT_ANNOTATED_CDS.
HASP, P15.16; INGJ.
MGD; MGI.1890219; Cdh23.
GO; GO:0005529; C:cilium; IDA.
GO; GO:0005529; C:cilium; IDA.
GO; GO:0005529; C:cilium; IDA.
GO; GO:0005529; C:cilium; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00112; CA; 26.
PROSITE; PS00232; CADHERIN 1; 17.
PROSITE; PS50268; CADHERIN 2; 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00028; cadherin; 27.
PRINTS; PR00205; CADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3354
3064
3085
3354
132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
```

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=S288C / AB972;

MEDIINE=97313267; PubMed=9169871;

MEDIINE=97313267; PubMed=9169871;

A Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Goffeau A., Hebling U., Heumann K.,

Benes V., Brueckner M., Goffeau A., Hebling U., Heumann K.,

Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter F.,

A Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,

Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,

A Portecelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rinke M.,

Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,

Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,

Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,

Hen nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";

Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION.
MEDLINE-21468387; PubMed=11583615;
Bassler J., Garadi V., Gadal O., Lessmann T., Petfalski E.,
Tallervey D., Lechner J., Hurt E.;
"Identification of a 608 preribosomal particle that is closely linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to nuclear export.", Mol. Cell 8:517-52(001).
-i- FUNCTION: May function as a nuclear chaperone and be involved in the assembly/disassembly of macromolecular complexes in the
                                                                               28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Midasin (MIDAS-containing protein).
MDN1 OR YLR106C OR L8004.13.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyceses.
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
PubMed=12102729;
Garbarino J.E., Gibbons I.R.;
"Expression and genomic analysis of midasin, a novel and highly conserved ApA protein distantly related to dynein.";
BMC Genomics 3:18-18(2002).
                                               PRT; 4910 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleus.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Contains 1 VMFA domain.
                                             STANDARD;
                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
                                        MDN1 YEAST
Q12019;
                                                 (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1; Length 335
Pred. No. 5.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAST/EI).
CAST/EI).
CAST/EI).
CAST/EI).
CAST/EI).
CAST/EI).
CAST/EI).
CAST/EI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLCNAC. . (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / FTIG=VGP 000648.
L -> P (IN STRAIN OR R -> V (IN STRAIN OR V -> V (IN STRAIN OR V -> V (IN STRAIN OR V -> V (IN STRAIN OR I -> V (IN STRAIN OR R -> T (IN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC.
(GLCNAC.
(GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC.
(GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                (GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                               GEONAC
GELONAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC.
(GLCNAC.
(GLCNAC.
(GLCNAC.
(GLCNAC.
  CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
CADHERIN
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           941
1001
1001
1001
11018
1171
1282
1315
1473
1651
1651
1667
1818
1857
1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11137
11236
2025
2025
22217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1001
112821
11331
11433
11667
11818
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
11885
                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
```

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified an expriction of its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). EMBL; U53876; AAB67548.1; -.
EWBL; Z73278; CAA97671.1; -.
PIR; S64942; S64942.
GermOnline; 142168; -.
SGD; S0004096; YiR106C.
GO; CO055634; C:nucleus; IDA.
InterPro; IPR00359; AAA\_ATPase\_
InterPro; IPR003959; AAA\_ATPase\_
InterPro; IPR003959; AAA\_ATPase\_
INTERPRO; IPR003959; AAA\_ATPASE\_
SMART; SM00382; AAA; 2.
SMART; SM00382; AAA; 6.
PROSTITE; PS50234; VWFP; 1.
Chaperone; ATP-binding; Repeat; Nuclear protein.

ö

Gaps

.

|:|||| |NDNWPT 2068 3 NNNWPT 8

2063

ò g ω

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license@agreennt (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                              ·
0
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                      Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDINDE-88087912; PubMed-6440122;
Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups are interdigitated within the VK locus.";
Within the VK locus.";
Nucleic Acids Res. 12:9229-9236(1984).
                                                                                                                                                                              ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG KAPPA CHAIN V-III REGION VG.
PRAMENOKK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMENOKK-2.
                                                                                                                                                   64.3%; Score 36; DB 1; Length 4910;
100.0%; Pred. No. 8e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.
                                                                                                                  4704 4899 VWFA.
4910 AA; 559302 MW; E4E873BEDF6E1E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2DE47CDA3A17D555 CRC64;
                                                                                                                                                                                                                                                                                                                   13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region VG precursor (Fragment).
                                     (POTENTIAL)
                          POTENTIAL)
                                                               POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X01668; -; NOT_ANNOTATED_CDS.
PIR, A01900; X3HUVG.
HSSP, P80362; 1NTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
ATP (POTE
POLY-LYS.
POLY-LEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF00047; ig; 1.
MRARI, SM00406, IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12575 MW;
                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                            STANDARD;
                         1090
1375
1754
2061
771
2907
48139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           >115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 J
                                                                                                                                                                                                                              2045 NNNWP 2049
                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                       3 NNNWP 7
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                         1083
1368
1747
                                                                                                   4136
                                                             2054
768
2904
                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
NON TER
SEQUENCE
NP_BIND
NP_BIND
NP_BIND
NP_BIND
NP_BIND
NP_BIND
                                                                                                                              SEQUENCE
                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                            KV3I HUM
P04433;
                                                                         DOMAIN
                                                                                                    DOMAIN
                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                     RESULT 11
  FT
FT
FT
FT
SQ
                                                                                                                                                                                                       ò
                                                                                                                                                                                                                             g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified annotate is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAINE=20365717; PubMed=10910347;
SIMEDLINE=20365717; PubMed=10910347;
SIMEDLINE=20365717; PubMed=10910347;
SIMEDON A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvaren L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barrones M.R.S., Barrones M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo L.E.A., Carraro D.M., Carrer H., Colaubo C., Costa M.C.R., Costa M.C.R., Costa-Neco C.M., Columbo L.L., Cristofani M.Dias-Neco E., Docena C., El-Dorry H., Raga J.S., Franca S.C., Franco M.C., Fronme M., Furlan L.R., A Garnicani M.P., Franca S.C., Franco M.C., Fronme M., Furlan L.R., Remper E.L., Kitajima J.P., A Cariser M.G., Goldman M.H.S., Gomes S.L., Gruber A., Hoheisel J.D., Junqueira M.H.S., Gomes S.L., Gruber A., Hobeisel J.D., Junqueira M.H.S., Lopes C.R., Machado J.A., Martins E.R., Martins E.M.F., Martins E.A., Martins
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
                                            .,
  1; Length 115;
                                                                                                                                                                                                                                                                                                (Rel. 41, Last sequence update)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                       224 AA
Score 35; DB
Pred. No. 25;
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003868; AAF82961.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                   DNA repair protein radC homolog.
RADC OR XF0148.
Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ONA repair; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIGRFAMS; TIGRO0608; radc; 1.
PROSITE; PS01302; RADC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_00018; -; 1.
InterPro; IPR001405; RadC.
Pfam; PF04002; RadC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD007415; RadC; 1.
Query Match 62.5
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                    109 QQRSNWP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                          1 QONNNWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                   16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=9a5c;
                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003
                                                                                                                                                                                                                                                    RADC XYLFA
Q9PGZ8;
                                                                                                                                                                                                           RESULT 12
                                                                                                                                    g
```

σ

RADC\_XYLFT

Matches

à

g

S

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12;

MEDLINE=97349980; PubMed=9205837;

MEDLINE=97349980; PubMed=9205837;

Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,

Itoh T., Kimus S., Kitegawa M., Makino K., Miki T., Mitsuhashi N.,

Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,

Mizobuchi K., Mori H., Nakade S., Satoh Y., Sivasundaram S.,

Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,

Yamagata S., Horiuchi T.,

Construction of a contiguous 874-kb sequence of the Escherichia coli

"Kl2 genome corresponding to 50.0-68 8 min on the linkage map and

TRI2 genome corresponding to 50.0-68,8 min on the linkage map and

II nalysis of its sequence features.";

DNA Res. 4:91-113(1997).

-I- FUNCTION: INVOLVED IN A MULTICOMPONENT BINDING-PROTEIN-DEPENDENT

TRANSPORT SYSTEM FOR GIYCINE BETAINE/L-PROLINE.

-I- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.

System permease family. CysTW subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-89197759; PubMed=2649479;
GONTISHARAT J.;
"Nucleotide sequence of the osmoregulatory proU operon of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN-RIZ / MGJ655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Flunkett G. III, Bloch C.A., Perna N.T., Burland V.
Blattner F.R., Flunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                  Bacteria; Protecobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                     Glycine betaine/L-proline transport system permease protein prow. Bacherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ecodene; EG10772; prow.
InterPro; IPR00515; BPD_transp.
Pfam; PF00528; BPD_transp; 1.
PR051TE; PS50928; ABC_TM1; 1.
Transport; Amino-acid_transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL) POTENTIAL.
                                    354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coli.";
J. Bacteriol. 171:1923-1931(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gowrishankar J.;
J. Bacteriol. 172:1165-1165(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M24856; AAA24428.1; -.
EMBL; AAC000352.1; -.
EMBL; D90881; BAA16543.1; -.
EIR; JS0129; MMECPW.
                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
DOMAIN 100
TRANSMEM 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                    ECOLI
PROW BROULD PROW B ACOLD PROW B B ACO DT O1-JAN DT O1-JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformetics and the EMBL outstation the between aboinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .<del>.</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=22421331, PubMed=12533478;

MISALINE=22421331, PubMed=12533478;

MIYAKI C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

MIYAKI C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

Takita M.A., Lemos B.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,

A Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,

A Marino C.L., Kimura E.T., Ferro B.S., Harakava R., Kuramae E.E.,

Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,

A Cucha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,

Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,

A Civerlo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kitajima J.P.; "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA repair protein radC homolog.

RADC OR PD0117.

Xylella fastidiosa (strain Temeculal / ATCC 700964).

Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales;
                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.5%; Score 35; DB 1; Length 224; 100.0%; Pred. No. 50; cive 0; Mismatches 0; Indels
                                                              DB 1; Length 224; 50;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF 00018; -; 1.
InterPro; IPR01405; RadC.
Pfam; PF04002; RadC; 1.
PROSITS; PS01302; RADC; 1.
DNA repair; Complete protecome.
SEQUENCE 224 AA; 24590 MW; E84351E63C8AF775 CRC64;
   224 AA; 24618 MW; 474351E63C880A5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fastidiosa.",
J. Bacteriol. 185:1018-1026(2003).
-!- FUNCTION: Involved in DNA repair (By similarity).
-!- SIMILARITY: Belongs to the radC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                224 AA.
                                                                                                                             0; Mismatches
                                                              62.5%; Score 35; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE012553; AA028016.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity luv..
France 5; Conservative
                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=183190;
                                                                                                                                                                                      4 NNWPT 8
                                                                                                                                                                                                                       4 NNWPT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 NNWPT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NWPT
                                                                                                                                                                                                                                                                                                                                                                                                          RADC XYLFT
Q87F21;
   SEQUENCE
                                                              Query Match
```

RESULT 14

ò

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia trachomatis.";
Science 282:754-759(1998)
-!- CATALNTIC ACTIVITY: Transfers a segment of a (1,4)-alpha-D-glucan
to a new 4-position in an acceptor, which may be glucose or (1,4)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-D-glucan.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the disproportionating enzyme family.
                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia Trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 1; Length 354;
Pred. No. 79;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003385; Glyco_hydro_77.
Pram; PF02446; 4A_glucanotrans; I.
TIGRPAMs; TIGROMS; I.
Transferase; Glycosyltransferase; Carbohydrate metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.5%; Score 35; DB 1; Length 527; Best Local Similarity 83.3%; Pred. No. 1.2e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
4-alpha-glucanotransferase (EC 2.4.1.25) (Amylomaltase)
(Disproportionating enzyme) (D-enzyme).
                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
D35F94A74E2779D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61453 MW; 52455D5E9ED2D46D CRC64;
                                                                                POTENTIAL.
PERIPLASMIC (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                              PERIPLASMIC (POTENTIAL).
PERIPLASMIC (POTENTIAL)
                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE001283; AAC67678.1; -. PIR; G71557; G71557.
                                                                                                                                                                                                                                                                                                                        37619 MW;
                                                                                                                                                                                                                                                                                                                                                                                62.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 QNNPWDTT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 QNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
SEQUENCE 527 AA;
                                                                                                                                                                                                                                                                                                                           354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=D/UW-3/Cx;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
MALQ CHITR
AC 084089;
DT 30-MAY-2000
DT 30-MAY-2000
DT 16-OCT-2001
DE 4-alpha-glucd
GN MALQ OR CTO8
CS CHIMMYDIA LTX
OC NCBL TAXID=87
CK NCBL TAXID=87
CK NCBLNE-9900
RX MEDINE-9900
RX MIChell W.P.
CC STRAIN-D/WW-
RY GRONGE EXPL
CC -1- CATALYTIC
CC -1- SIMILARI
CC -1- 
                                                                                                               DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                  TRANSMEM
DOMAIN
TRANSMEM
                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                              FRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                            DOMAIN
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

```
|:|||
186 NHWPTT 191
       d
```

6, 2004, 16:30:32 Search completed: October Job time: 7.52632 secs

4 NNWPTT 9

Appli 11, Appli 11, Appli 11, Appli 113, Appl 113, Appl 127, Appl 129, Appl 129, Appl 129, Appl 129, Appl 123, Appl 123, Appl 123, Appl 123, Appl 123, Appl 123, Appl 124, Appl 127, Appl 137, Appl 136, Appl 137, Appl 137, Appl 136, Appl 137, Appl 137, Appl 137, Appl 137, Appl 138, Appl 137, Appl 137, Appl 138, Appl 137, Appl 138, Appl 138, Appl 137, Appl 138, Appl 138, Appl 139, Appl 131, Appl

Sequence 1 Sequence 1 Sequence 2 Sequence 8 Sequence 1

Sequence

Sequence 1 Sequence 1 Sequence 2

Sequence Sequence Sequence Sequence Sequence

Sequence 1 Sequence 1 Sequence 6 Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq

Sequence:

Run on:

Database

```
US-90-798-809-36

Sequence 36, Application US/09798689

Publication No. US20030103973A1

GENERAL INFORMATION:

APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.

TITLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE SPERENCE: Sequence Listings 1-41 for 381-25 CIP
FILE REPERENCE: Sequence Listings 1-41 for 381-25 CIP
CURRENT APPLICATION NUMBER: US/09/798,689

CURRENT APPLICATION NUMBER: US/09/101.163

PRIOR APPLICATION NUMBER: 08/967,113

PRIOR FILING DATE: 1999-09-22

PRIOR FILING DATE: 1999-09-03

PRIOR FILING DATE: 1996-09-03

PRIOR FILING DATE: 1996-09-03

PRIOR FILING DATE: 1994-10-20

PRIOR FILING DATE: 1994-10-20

PRIOR FILING DATE: 1994-10-20

PRIOR FILING DATE: 1994-10-10

PRIOR FILING DATE: 1994-10-20

PRIOR FILING DATE: 1994-10-20

PRIOR FILING DATE: 1994-10-20

PRIOR FILING DATE: 1994-10-10

PRIOR FILING DATE: 1994-10-10

PRIOR FILING DATE: 1994-10-10

PRIOR PRIOR PRIOR NUMBER: 08/196,041

PRIOR PRIOR PRIOR DATE: 1994-10-10

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 56; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                     US-10-374-531-11

US-10-374-531-11

US-10-374-531-15

US-10-374-531-13

US-10-453-698-129

US-10-453-698-129

US-10-453-698-129

US-10-453-698-129

US-10-453-698-129

US-10-453-698-129

US-10-308-817-139

US-10-308-817-139

US-10-251-0858-123

US-10-737-252-132

US-10-737-252-133

US-10-737-253-133

US-10-737-253-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
122777
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
122777
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
122777
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
12277
122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OONNNWPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mouse US-09-798-689-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
US-09-798-689-36
₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36, Appl
Sequence 112, Appl
Sequence 112, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 27, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                           October 6, 2004, 16:34:15; Search time 56.0526 Seconds (without alignments) 51.669 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: Ggn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-798-689-36
US-00-996-954B-12
US-10-374-600-112
US-10-374-600-114
US-10-374-600-20
US-10-374-600-22
US-10-374-600-23
US-10-374-600-23
US-10-374-600-23
US-10-374-600-23
US-10-374-600-23
US-10-374-600-23
US-10-374-600-5
US-10-374-600-5
US-10-374-600-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1351062 segs, 321799191 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                             US-09-635-974A-12
56
1 QONNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
```

ö

Gaps

; 0

Result

```
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QONNNWPIT 9
                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                               RESULT 2
US-09-96-954B-12
US-09-96-954B-12
Sequence 12, Application US/099694B
Publication No. US20030157104A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
With Epidermal Growth Factor Receptor Antagonists
TITLE OF INVENTION:
WITH APPLICATION NUMBER: US/09/996,954B
CURRENT APPLICATION NUMBER: US/09/996,954B
PRIOR APPLICATION NUMBER: 09/374,028
PRIOR FILING DATE: 08-13-1999
PRIOR APPLICATION NUMBER: 09/374,028
PRIOR APPLICATION NUMBER: 09/312,284
PRIOR PELING DATE: 08-13-1999
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 112, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: IMClone Systems Incorporated, et al.
ITLE OF INVENTION: ANTIBODY AND ANTIBODY FRACMENTS FOR INFIBERAL THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 56; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10004

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/08/973,065C
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens-Rodent Chimera
US-09-996-954B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon STREET: One Broadway CITY: New York STATE: New York COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QONNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QONNNWPIT 9
QQNNNNWPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-10-374-600-112
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: IMCIONE Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR
INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDION TIPE: DISRECTE 3.5 INCH 1.44 FOR COMPUTER: IBM COMPUTED B. COMPUTER: IBM COMPUTED B. SOFTWARE: WORDSERVED COURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-F6b-2003
CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1996
APPLICATION NUMBER: DCT/US96/09847
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:

NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 31,995
  11245/46003
                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
HYPOTHETICAL: No Peptide
FRAGMENT TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-10-374-531-112
Sequence 112, Application US/10374531
Sequence 112, Application No. US20040006212A1
SENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                  (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
                                                                          425-5288
                                                                                                                                                    LENGTH: 9 amino acids
                                                                       TELEFAX: (212) 425-52 INFORMATION FOR SEQ ID NO: 112: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: One Broadway
```

```
RESULT 7
US-10-374-600-20
                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                       ö
                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 114, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
GENERAL INCOMATION:
APPLICANT: Inclone Systems Incorporated, et al.
APPLICANT: Inclone Systems Incorporated, et al.
ITTLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 56; DB 12; Length 107; larity 100.0%; Pred. No. 0.18; Conservative 0; Mismatches 0; Indels
                                                                                                                                            Length 9;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1995
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REPERENCE/DOCKET NUMBER: 11245/46003
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
HYPOTHETICAL: NO FRAGMENT TYPE: peptide
HYPOTHETICAL: NO FRAGMENT TYPE: internal
SEGUNCE DESCRIPTION: SEQ ID NO: 112:
US-10-374-531-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX: (212) 425-5288
SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Ke
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                                                                                                                                                                                                   1 QONNNWPIT
                                                                                                                                                                                                                                                                          1 QONNNWPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                      US-10-374-600-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-10-374-600-114
                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                          셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 56; DB 15; Length 107; Best Local Similarity 100.0%; Pred. No. 0.18; Matches 9; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                        Sequence 114, Application US/10374531
Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INVENTION: IMHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/10374600
; Publication No. US20030224001A1
; Publication No. INCOMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: ANTIBODY AND ANTIBODY FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: 12.0RM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MG-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown>
PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 10-Mar-1996
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UN-1996
APPLICATION NUMBER: US 06/482,982
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborah & Somerville
REGISTRATION NUMBER: 31,995
ATTORNEY/AGENT INFORMATION:
NAME: DEBOSTAR A. SOMERVILLE
REGISTRATION NUMBER: 31,995
TELECOMMUNICATION NUMBER: 31,995
ATTORNEY/AGENT UNMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-374-531-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: not relevant
TOPOLOGY: not relevant
ULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 107 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 425-5
INFORMATION FOR SEQ ID NO: 114
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York COUNTRY: US
89 QQNNNNPTT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 QONNNWPTT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10004
```

ð

Indels

0; Mismatches

```
RESULT 9
(2-10-3-4-600-23)
(2-10-3-4-600-23)
Sequence 23, Application US/10374600)
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: ImClone Systems Incorporated, et al.
ITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INTIBUTION THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10004
COMPUTER READBBLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/USS6/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 31,995
TELECOMMUNICATION INFORMATION:
TELECHONE (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/374,600 FILING DATE: 25-Feb-2003 CLASSIFICATION: <UNKnown>PRIOR APPLICATION DATA:
                                                                                                          APPLICATION NUMBER: US/10/374,600 FILING DATE: 25-Feb-2003 CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 22: US-10-374-600-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                         SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 QONNWWPTT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QQNNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 56; DB 12; Length 113; Best Local Similarity 100.0%; Pred. No. 0.19; Matches 9; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: IMClone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
INHIBITING THE GROWTH OF TUMORS CONDENS. 120
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/08/973,065C FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/462,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEPHONE: (212) 425-5288
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Peb-2003
CLASSIFICATION: <UNKNOWD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDESS: not relevant
TOPOLOGY: not relevant
TOPOLOGY: not relevant
HYPOTHETICAL: NO
PRAGNENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-374-600-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
                                                                                    ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                          COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 113 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 QONNNWPIT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QONNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-374-600-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

ô

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 56; DB 15; Length 113; Best Local Similarity 100.0%; Pred. No. 0.19; Matches 9; Conservative 0; Mismatches 0; Indels

    Sequence 22, Application US/10374531
    Publication No. US20040006212A1
    GENERAL INFORMATION:
    APPLICANT: ImClone Systems Incorporated, et al.
    IITLE OF INVENTION:
    INTLE OF INVENTION:
    INHIBITING THE GROWTH OF TUMORS
}

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/10/374,531
FILING DATE. 25-F6b-2003
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION: UNKNOWN>
RPLING DATE: 19-MAT.
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-MAT.1998
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DE0-1995
APPLICATION NUMBER: US 08/482,982
FILING DATE: 15-DE0-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUBER: 11245/46003
TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEPRAS: (212) 425-5288
                                                                                                                        LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECTLE TYPE: peptide HYPOTHETICAL: NO FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                    425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 113 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
        TELEFAX: (212) 425-5;
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 QONNWWPTT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QONNNWETT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-374-531-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

100.0%; Score 56; DB 12; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/10374531
Sequence 20, Application US/20040006212A1
Publication No. US20040006212A1
GENERAL INFORMATION:
APPLICANT: Imclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFFWARE: Wordperfect CURRENT APPLICATION DATA:
FILING DATE: 07-UUN-1996

APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UUN-1995

APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 31,995

REFERENCE/DOCKET NUMBER: 31,995

REFERENCE/DOCKET NUMBER: 31,995

REFERENCE/DOCKET NUMBER: 31,995

REFERENCE/DOCKET NUMBER: 31,995

REFERENCE/OCKET NUMBER: 31,995

TELEPHONE: (212) 425-7200

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR DATE: 25-Feb-2003
CLASSIFICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION OF CHARDOWN>
PRIOR APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Max-1998
APPLICATION NUMBER: US/08/973,065C
FILING DATE: 07-UW-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UW-1995
FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKST NUMBER: 11245/46003
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | JENGTH: 113 amino acids | JENGTH: 115 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 QONNNWPTT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QQNNNNNDTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-374-531-20
```

δ d

```
ZIP: 10004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 QONNNWPTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DONNNWPTT
                                                                                                                                                                                                                                                                                                      COUNTRY:
                  JS-10-374-600-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·.
                                                                                  .
0
                                                                                                                                                                                                                     RESULT 12
US-10-374-531-23
is Sequence 23, Application US/10374531
j Publication No. US20040006212A1
j Publication No. US20040006212A1
j GENERAL INFORMATION:
j APPLICANT: InClone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR TITLE OF INVENTION:
120
                                    Query Match
100.0%; Score 56; DB 15; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 100.0%; Score 56; DB 15; Length 113; Similarity 100.0%; Pred. No. 0.19; 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOPERATING SYSTEM: MS-DOS CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-UUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-UUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/ABONT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 31,995
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | LENGTH: 113 amino acids | LENGTH: 113 amino acids | TYPE: amino acids | TYPE: amino acids | STRANDEDNESS: not relevant | TOPOLOGY: not relevant | TOPOLOGY: not relevant | TOPOLOGY: not relevant | HYPOTHETICAL: NO | FRAGMENT TYPE: internal | SEQUENCE DESCRIPTION: SEQ ID NO: 23: US-10-374-531-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/374,531
FILING DATE: 25-Feb-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STRIES: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 QONNWPTT 103
                                                                                                                                                                       95 CONNINWPTT 103
                                                                                                                              1 QONNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QONNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
US-10-374-531-22
                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
(2-10-37-4600-11)
/Sequence 11, Application US/10374600
/ Publication No. US20030224001A1
/ Publication No. US20030224001A1
/ GENERAL INFORMATION:
/ APPLICANT: ImClone Systems Incorporated, et al.
/ TITLE OF INVENTION: ANTIBODY FRAGMENTS FOR TITLE OF INVENTION: INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 127;
Sequence 5, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: IMCION: Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INHIBITING THE GROWTH OF TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible compatient SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 31,995
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 56; DB 12; 100.0%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
FLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: internal
;
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-374-600-5
                                                                                                                                                   NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENČE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 127 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 425-5
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
```

```
100.0%; Score 56; DB 12; Length 127; 100.0%; Pred. No. 0.21;
                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
FILING DATE: 19-Mar 1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
    APPLICATION NUMBER: US/10/374,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: internal
;
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-374-600-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6, 2004, 17:09:06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                        FILING DATE: 25-Feb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 CONNNWPTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: October Job time: 57.0526 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 56; DB 12; Length 127; 100.0%; Pred. No. 0.21; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/10374600
Publication No. US20030224001A1
GENERAL INFORMATION:
APPLICANT: Inclone Systems Incorporated, et al.
TITLE OF INVENTION: ANTIBODY AND ANTIBODY FRAGMENTS FOR INTELLIBED INTE
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette 3.5 inch 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/973,065C
PILING DATE: 19-Mar-1998
APPLICATION NUMBER: PCT/US96/09847
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 08/482,982
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/573,289
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Deborah A. Somerville
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 11245/46003
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,600
FILING DATE: 25-Feb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO FERGMENT TYPE: internal
US-10-374-600-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOCY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 425-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELEFAX: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: One Broadway CITY: New York
STREET: One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 QQNNNNNPTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QONNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-10-374-600-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

Gaps

. 0

0; Indels

This Page Blank (uspto)

Sequence

Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

```
RESULT 1

US-07-956-399-2

j Sequence 2, Application US/07956399

j Patent No. 587677

GENERAL INFORMATION;

APPLICANT: SHIMAWURA, TOSHIRO

APPLICANT: HAMUNO, JUNJI

TILLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY

TITLE OF INVENTION: CHAINS OF IL-2 RECEPTORS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS: 4

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Alington

STATE: Virginia

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

ABDION TYPE: Floppy disk
COMPUTER: IS PROPY disk
COMPUTER: IS PROPY disk
COMPUTER: IS PROPY disk
COMPUTER: IS PROPY disk
COMPUTER: IS PROPED COMPUTED:
COMPUTER: IS PROPED COMPUTED:
COMPUTER: IS PACENTIN RELEASE #1.0, Version #1.25
SOSTWARE: PACENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA: US /07/956,399
FILING DATE: 19921005
CLASSIFICATION NUMBER: US /07/956,399
ATTORNEY/AGBNT INFORMATION:
NAME: Oblon, No. 587617man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-586-0
TELEPHAN: (703) 413-320
TELEPHAN: (703) 413-320
TELEPHAN: (703) 413-320
TELEFAX: (703) 413-320
TELEFAX: CASEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENGTH: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENGTH: 240 amino acids
US-08-436-463-21

US-09-2463-18

US-09-339-92A-86

US-09-339-92A-86

US-08-90-166-86

US-08-436-463-19

US-08-436-463-19

US-07-634-278-63

US-07-634-278-63

US-08-477-728-63

US-08-477-728-83

US-08-477-728-83

US-08-477-728-83

US-08-474-040-63

US-08-474-040-63

US-08-474-040-63

US-08-474-040-63

US-08-474-040-63

US-08-474-040-63

US-08-474-040-63

US-08-474-040-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
80.4%; Score 45; DB 2
Best Local Similarity 77.8%; Pred. No. 6.6;
Matches 7; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 240 amino acids
AMINO ACID
                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LIAMNNNOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-956-399-2
       444mmmmmmmmmmmmmmmm
       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                             October 6, 2004, 16:24:54 ; Search time 15:9474 Seconds (without alignments) 29:135 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34, Sequence 34, Sequence 34, Sequence 34, Sequence 55, Sequence 55, Sequence 55, Sequence 4, A Sequence 4, A Sequence 6, A Sequence 6, A Sequence 10, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Sequence 8, Asequence 8, As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4,
Sequence 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued Patents Ah:*

/ Goll 6 / ptodate 2 / iaa / 54 COMB.pep: *

/ Goll 6 / ptodate 2 / iaa / 55 COMB.pep: *

/ Goll 6 / ptodate 2 / iaa / 65 COMB.pep: *

/ Goll 6 / ptodate 2 / iaa / 65 COMB.pep: *

/ Goll 6 / ptodate 2 / iaa / pcrus COMB.pep: *

/ Goll 6 / ptodate 2 / iaa / pcrus COMB.pep: *

/ Goll 6 / ptodate 2 / iaa / pcrus COMB.pep: *

/ Goll 6 / ptodate 2 / iaa / pcrus COMB.pep: *

/ Goll 6 / ptodate 2 / iaa / pcrus COMB.pep: *
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-956-399-2
US-09-456-090A-84
US-07-654-278-34
US-08-477-728-34
US-08-477-728-34
US-08-477-728-34
US-08-477-728-34
US-08-478-17.85-55
US-08-485-246A-55
US-08-485-246A-55
US-08-476-1768-4
US-08-476-1768-4
US-08-476-1768-4
US-08-476-1768-4
US-08-476-1768-6
US-08-477-1768-6
US-08-477-1768-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                               389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                          US-09-635-974A-12
56
1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length
                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                   OM protein
                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                     Run on:
```

ö

Gaps

ö

Indels

ô

Gaps

. 0

```
/note= "Amino acid sequence of the light chain for humane Lay antibody."
                                                                                                              Score 44; DB 2; Length 239;
Pred. No. 9.4;
                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CO., Man. Sung
APPLICANT: CO., Man. Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: ANDOLET, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PULGASIFICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-82P-1990
FILING DATE: 28-82P-1990
FRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-F2B-1989
FRIING DATE: 13-F2B-1989
FRIING DATE: 28-D2C-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-D2C-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                       RESULT 4
18-07-634-278-34
Sequence 34, Application US/07634278
Patent No. 5530101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                       TOPOLOGY: linear; MOLECULE TYPE: protein US-07-956-399-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
US-07-634-278-34
                                                                                                                                                                                                                                                                90 QQTNTWPTT 98
                                                                                                                                                                                                                  1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
LOCATION: 1..107
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUEEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                             원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/07956399
Patent No. 5876717
GENERAL INFORMATION:
APPLICANT: SHIMAWIRA, TOSHIRO
APPLICANT: TAKI, SHINAUKE
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
TITLE OF INVENTION: CHAINS OF IL-2 RECEPTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                      Sequence 84, Application US/09456090A

Sequence 84, Application US/09456090A

Patent No. 6680209

SGENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Gray, Jeff
TITLE OF INVENTION:
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
TITLE OF INVENTION: UNDER: US/09/456,090A

CURRENT FILICATION NUMBER: US/09/456,090A

CURRENT FILICATION NUMBER: US/09/456,090A

CURRENT FILICATION NUMBER: US/09/456,090A

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 84

LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 4; Length 224;
Pred. No. 9.8;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,399
FILING DATE: 19921005
CLASSIPICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5876717man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-586-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 118-2000
TELECOMMUNICATION 118-3000
TELECAS: 248655 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TENERY: 239 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
CTHER INFORMATION: M2-32L
US-09-456-090A-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 QQRINIWPLT 97
  90 QTNSWPTT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
ADDRESSEE:
                                                                  RESULT 2
US-09-456-090A-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-07-956-399-4
g
```

à

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1.107

OTHER INFORMATION: /note= "Amino acid sequence of the OTHER INFORMATION: light chain for humane Lay antibody."
US-08-474-0460-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.0%; Score 42; DB 1; Length 107; Best Local Similarity 77.8%; Pred. No. 8.6; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                   Sequence 34, Application US/08474040

Patent No. 563761

GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOCLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOwnsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: REALBLE FORM disk MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/474,040 FILING DATE: 07-JUN-1995 CLASSIPICATION: 536 PRIOR APPLICATION NUMBER: US 07/634,278 FILING DATE: 12-DEC-1990 APPLICATION NUMBER: US 07/530,274 FILING DATE: 12-DEC-1990 APPLICATION NUMBER: US 07/310,252 FILING DATE: 13-FEB-1990 FRIOR APPLICATION NUMBER: US 07/290,975 FILING DATE: 13-PEC-1989 FRIOR APPLICATION NUMBER: US 07/290,975 FILING DATE: 28-DEC-1980 FRIOR APPLICATION NUMBER: US 07/290,975 FILING DATE: 28-DEC-1980 ATCORNEY/AGENT INFORMATION: NAME: Smith, William M REGISTRATION NUMBER: 11823-002600 TELECOMMUNICATION INPORMATION: TELECOMMUNICATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue STREET: 219 Lytton Avenue STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                     89 QQYNNWPPT 97
         1 QONNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                               RESULT 6
US-08-474-040-34
         ò
                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Amino acid sequence of the light chain for humane Lay antibody."
                                                                                                                                                                                                                                                                                US-08-147-728-34

US-08-477-728-34

Sequence 34, Application US/08477728

Sequence 34, Application US/08477728

September 100-1585089

GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
      DB 1; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 75.0%; Score 42; DB 1; Length 107; Best Local Similarity 77.8%; Pred. No. 8.6; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 94111
SALID: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERAITMG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-EEP-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 13-FEB-1989
ATTORNEY/AGENT INFORMATION:
FILING DATE: 26-DEC-1988
ATTORNEY/AGENT INFORMATION:
FELERPACE SMICH NUMBER: 11823-002600
TELEFAX: (415) 326-2420
INFORMATION FOR EQUID NO: 34:
FELERPAX: (415) 326-2420
INFORMATION FOR EQUID NO: 34:
FELERPAX: (415) 326-2420
INFORMATION PROBRES: SINGLE
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TTORINGY: unknown
                                                                     0; Mismatches
      Score 42;
Pred. No.
      75.0%;
Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME KEY: Protein
LOCATION: 1..107
OTHER INFORMATION: /
                                                                                                                                                                                         89 QOYNNWPPT 97
                                                                                                                              1 QONNWWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-477-728-34
```

ö

89 QQYNNWPPT 97

```
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Amino acid sequence of the light chain for humane Lay antibody."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.0%; Score 42; DB 1; Length 107; Best Local Similarity 77.6%; Pred. No. 8.6; Matches 7; Conservative 0; Mismatches 2; Indels
                                    Sequence 34, Application US/08487200

Patent No. 5693762

GENERAL INFORMATION:

APPLICANT: CO. Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: COELINGH, Kathleen L.

APPLICANT: CELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS

NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRIES 94301

ZIF: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPUTER: COMPATIBLE
COMPUTER: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200

TILING DATE: 7-474
                                                                                                                                                                                                                                                                                                                                                 Townsend and Townsend and Crev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 7-JUN-1995
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FSB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FSB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: SE-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REFERENCE/DOCKET NUMBER: 11823-00261
FIRESCHORLOWER: 130,223
REFERENCE/DOCKET NUMBER: 11823-00261
FIRESCHORLOWERTION INFORMATION:
MATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 11823-00261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2402
INPORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                      STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 107 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..107
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
RESULT 7
US-08-487-200-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-487-200-34
```

```
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Amino acid sequence of the light chain for humane Lay antibody."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.0%; Score 42; DB 3; Length 107; 77.8%; Pred. No. 8.6; 2; Indels iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                           APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLLINGH, Micholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING JATE

FILING PAPELICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

FILING DATE:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME:

RETERENCE/DOCKET NUMBER:

TELEPONMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPONMUNICATION INFORMATION:

TELEPONMUNICATION NUMBER:

TELEPHONE:

(ALS)

ACCOMMUNICATION NUMBER:

TELEPHONE:

(ALS)

TELEPHONE:

(ALS)

ACCOMMUNICATION INFORMATION:

ACCOMMUNICATION INFORMATION:

TELEPHONE

ACCOMMUNICATION INFORMATION:

ACCOMMUNICATION INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: Galifornia
COUNTRY: 01
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: 
                                                                                                                     Sequence 34, Application US/08484537 Patent No. 6180370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
LOCATION: 1..107
OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
STREET: 37
RESULT 8
US-08-484-537~34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-484-537-34
```

QONNNWPTT 9

```
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 55, Application US/08485246A
Patent No. 6072035
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
CONTRAINED TO THE CONTRAINED TO THE COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APELICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424
RELOR APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 606718AK, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELEPAX: (908) 277-4106
INFORMATION EN OR SEQ ID NO: 55:
ENDUCTH: 9 amino acids

LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTEXT ON THE STATE OF STATES ADDRESSEE: No. 6072035artis Patent Department STREET: 59 Route 10 CITY: East Hanover STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
FILING DATE: 27-SEPTEMBRR-1993
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBRR-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBRR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 3;
Pred. No. 3e+05;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-127-721A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QOSDSWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-08-485-246A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                         USERIOR TO THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NESULI 17-721A-55

Sequence 55, Application US/08127721A

Patent No. 6066718

GENERAL INFORMATION:

APPLICANT: Hardman, No. 6066718man

APPLICANT: Saldanha, Joser, Frank

TITLE OF INVENTION: Reshaped monoclonal antibodies against an

TITLE OF INVENTION: immunoglobulin isotype

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6066718artis Patent and Trademark Department

STREET: S9 Route 10

CITY: East Hanover

STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 2;
Pred. No. 3e+05;
3; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 73.2
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QONNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                   JS-08-476-176B-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-476-176B-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
```

ò d

ö

Gaps

```
GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEGUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 3; Length 106;
Pred. No. 12;
3; Mismatches 0; Indels
                                                                            Sequence 4, Application US/09296595A
Sequence 4, Application US/09296595A
Sequence 4, Application US/09296595A
Sequence 4, Application US/09296595A
GENERAL INFORMATION
SEQUENCE 5, APPLICANT: WINTRIED S.
APPLICANT: WEALOPOULOU, EVANGELIA
APPLICANT: WEALOPOULOU, EVANGELIA
APPLICANT: WEALOPOULOU, EVANGELIA
APPLICANT: SCH-1576 D1
CURRENT APPLICATION NUMBER: US/09/296,595A
CURRENT APPLICATION NUMBER: US/09/296,595A
CURRENT PILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: 08/800,198
EARLIER PILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 18
SOSTWARE PARENT NET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: Bast Hanover
STATE: New Jersey
COUNTRY: USA
ZID: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTONNEY/AGBWT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08476176B Patent No. 5958708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 73.2
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 QQSDSWPTT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QONNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SEQ ID NO 4
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-296-595-4
                                                                       US-09-296-595-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.2%; Score 41; DB 2; Length 106; 66.7%; Pred. No. 12; trive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08800198
; Patent No. 5942602
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WCLS, WINERIED S.
APPLICANT: WAKALOPOULOU, EVANGELIA
APPLICANT: SCHMIDT, MATHIAS
; APPLICANT: SCHMIDER, DOUGLAS
; TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
                                                                                                                                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,198
FILING DATE: 13-FEB-1997
CLASSIPICATION: 530
                                                                                                                                                                                                                                                                                Query Match 73.2%; Score 41; DB 3; Best Local Similarity 66.7%; Pred. No. 3e+05; Matches 6; Conservative 3; Mismatches
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LASSIFICATION: 530

ATTORNEY AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: 367
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-243-6410
INPORMATION FOR ESQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acide
STRANDEDNESS:
TOPONIATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . peptide
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                         / MOLECULE TYPE: protein US-08-485-246A-55
                                                                                                                                                                                                                                                                                                                                                                             1 QONNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                      1 QOSDSWPTT 9
                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 2200 CLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-800-198-4
```

(908) 277-4306

89 QQSDSWPTT 97

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-US-127-721A-4

Sequence 4, Application US/08127721A

Sequence 4, Application US/08127721A

Sequence 1, No. 6066718

GENERAL INPORATION:

APPLICANT: Hardman, No. 6066718man

APPLICANT: Rolbinger, Frank

APPLICANT: Saldanha, Jobse

ITITLE OF INVENTION: immunoglobulin isotype

CORRESPONDENCE ADDRESS: 55

CORRESPONDENCE ADDRESS: 55

CORRESPONDENCE ADDRESS: 55

CONTURE: Bast Hanover

STATE: No. 606671884.De

COMPUTER: READBLE FORM:

STATE: MW JETSEY

COMPUTER: READBLE FORM:

STATE: MW JETSEY

COMPUTER: EAPPERMER-1993

INTING OFTER STETEMBER-1993

CLASSIFICATION NUMBER: US/08/127,721A

FILING DATE: 2-SEPTEMBER-1993

FILING DATE: 2-SEPTEMBER-1993

FILING DATE: 2-SEPTEMBER-1993

FELICATION NUMBER: 3-4-19276/A/P2/CIP

TELEFROME NUMBER: 3-4-19276/A/P2/CIP

TELEFROME (908) 277-510

TYPE: amino acids

TYPE: maino acids

TYPE: maino acids

TYPE: maino acids

TYPE: maino acids

TYPE: MULL TYPE: non-ainomental and transpectors are acids

TYPE: maino acids

TYPE: maino acids

TYPE: MULL TYPE: non-ainomental and transpectors are acids

TYPE: non-aino-acids

TYPE: maino acids

TYPE: maino acids

TYPE: non-aino-acids

TYPE: maino acids

TYPE: non-aino-acids

TYPE: non-acids

TYPE: non-acids

TYPE: non-acids

TYPE: non-acids

TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                      Query Match 73.2%; Score 41; DB 2; Length 107; Best Local Similarity 66.7%; Pred. No. 12; Matches 6; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.2%; Score 41; DB 3; Length 107; 66.7%; Pred. No. 12; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                     SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66,7
Matches 6; Conservative
                                                                                                                                       TOPOLOGY: linear;
MOLECULE TYPE: protein US-08-476-176B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-127-721A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 QQSDSWPTT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QQNNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

Search completed: October 6, 2004, 16:36:34 Job time : 16.9474 secs

89 QQSDSWPTT 97

1 QQNNNNWPIT 9

ઠે

This Page Blank (uspto)

October 6, 2004, 16:20:48; Search time 45.4737 Seconds (without alignments) 55.921 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 1586107 seqs, 282547505 residues OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 US.-09-635-974A-12 56 1 QQNNNWPTT 9 Scoring table: Title: Perfect score: Searched: Sequence: Run on:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* A\_Geneseq\_29Jan04:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|            | Description    | Aav59316 Light cha | Aab37957 Anti-EGFR | Aau77789 Mouse lig | 6          | Н        | -        | Kappa 1  | _        | 3 Kappa 1 | a        |          | Aaw05140 scFv2(225 | Aaw05139 BCFv2 (FRP | Aaw05141 scFv2 (FRP | Aar32129 Anti-IL2R | Aar34510 Fv(TU27). | Aab99396 Human int | Aab75029 Anti-IL8 |          | Abr54897 Light cha | Abr54906 Light cha |          | Light    | 6 Light | Abr54891 Light cha |
|------------|----------------|--------------------|--------------------|--------------------|------------|----------|----------|----------|----------|-----------|----------|----------|--------------------|---------------------|---------------------|--------------------|--------------------|--------------------|-------------------|----------|--------------------|--------------------|----------|----------|---------|--------------------|
| SUMMARIES  | CI             | AAY59316           | AAB37957           | AAU77789           | AAW08949 - | AAW08948 | AAW08945 | AAW08941 | AAW08946 | AAW08943  | AAW05133 | AAW05135 | AAW05140           | AAW05139            | AAW05141            | AAR32129           | AAR34510           | AAB99396           | AAB75029          | AAR34511 | ABR54897           | ABR54906           | AAB69657 | ABR54895 | 8       | ABR54891           |
|            | DB             | <u>.</u> 6         | 4                  | 'n                 | 7          | 7        | N        | (7)      | ~        | 0         | ~        | ~        | N                  | 7                   | ~                   | ~                  | ~                  | 4                  | 4                 | 7        | ø                  | 9                  | 4        | 9        | 9       | ø                  |
|            | Length         | . 0                | σ                  | σ                  | 107        | 107      | 127      | 127      | 127      | 127       | 240      | 651      | 892                | 892                 | 1020                | 107                | 240                | 224                | 224               | 239      | 107                | .108               | 107      | 107      | 107     | 107                |
| ole<br>ole | Query<br>Match | 100.0              | 100.0              | 100.0              | 100.0      | 100.0    | 100.0    | 100.0    | 100.0    | 100.0     | 100.0    | 100.0    | 100.0              | 100.0               | 100.0               | 80.4               | 80.4               | œ.                 | ω,                | 78.6     | ģ                  | 9                  | 75.0     | 75.0     |         | 75.0               |
|            | Score          | 56                 | 56                 | 26                 | 26         | 56       | 56       | 26       | 26       | 56        | 56       | 26       | 56                 | 26                  | 26                  | 45                 | 45                 | 44                 | 44                | 44       | 43                 | 43                 | 42       | 42       | 42      | 42                 |
|            | Result<br>No.  |                    | 7                  | m                  | 4.         | ស        | 9        | 7        | 80       | σ         | 10       | 11       | 12                 | 13                  | 14                  | 15                 | 16                 | 17                 | 18                | 19       | 20                 | 21                 | 22       | 23       | 24      | 25                 |

| Abr54899 Light cha Abr54882 Light cha Abr54883 Light cha Abr64893 Light cha Adc61017 Human ant Adc61017 Human ant Adc99777 Anti-huma Adc99805 Anti-huma Adc99805 Anti-huma Add05482 Anti-huma Add05482 Anti-humC1 Add05482 Anti-humC1 Add13784 vKappa ex Adc61102 Human ant Adc61102 Human ant Adc61102 Human ant Adc61107 Human ant | 2537<br>254<br>254<br>254                                |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------|
| ABR54899 ABR54882 ABR54883 ABR54883 ABC61017 ADC61017 ADC9777 ADC95777 ADD05409 ADD05381 ADD05381 ADD05102 ADD05784 ADC61100 AAM77557 AAM77557                                                                                                                                                                                       | ABG59199<br>ABG46586<br>ABP45257<br>ABP45941<br>ADD13794 |
| 000000000000000000000000000000000000000                                                                                                                                                                                                                                                                                              |                                                          |
| 10000000000000000000000000000000000000                                                                                                                                                                                                                                                                                               | H H H H H H H H H H H H H H H H H H H                    |
| 75.0                                                                                                                                                                                                                                                                                                                                 | ດິດວິດ                                                   |
| 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                                | 4444                                                     |
| 0 7 8 0 0 1 1 2 m 4 1 1 0 7 1 8 0 0 0 1 2 m 4 1 1 0 7 1 8 0 0 0                                                                                                                                                                                                                                                                      | 4 4 4 4 4<br>ዛሪይፋኒ                                       |

| **  |  |
|-----|--|
| ິດ  |  |
| E   |  |
| 2   |  |
| 쁘   |  |
| 2   |  |
| 4   |  |
| O   |  |
| ч   |  |
| H   |  |
| AT. |  |

Hypervariable region, complementarity determining region, CDR, tumour, single chain antibody, growth inhibitor, human, tumourigenesis, therapy, protein receptor tyrosine kinase, light chain. Robert F, Buchsbaum DJ; Light chain hypervariable region, CDR3. AAY59316 standard; peptide; 9 AA. 98US-00079612. 98US-0085613P. 98US-00206138. 99WO-US010741. (IMCL-) IMCLONE SYSTEMS INC. (UABR-) UAB RES FOUND. 07-MAR-2000 (first entry) Waksal HW, Saleh MN, WPI; 2000-062440/05. N-PSDB; AAZ48630. 15-MAY-1998; 15-MAY-1998; 07-DEC-1998; WO9960023-A1 14-MAY-1999; 25-NOV-1999. AAY59316; Mus sp. RESULT 1 AAY59316 ID AAY5 

Treatment of human tumors, using a combination of radiation and a non-radiolabeled protein receptor tyrosine kinase inhibitor.

Disclosure; Page 15; 31pp; English.

This sequence is the hypervariable region CDR3 (complementarity determining region 3) of the light chain of a single chain antibody derived from the murine antibody 25. The invention relates to a method for inhibiting the growth of tumours in human patients by treating with an effective amount of a combination of radiation and a non-radiolabelled protein receptor tyrosine kinase (PRTX) inhibitor, the overexpression of which can lead to tumourigenesis. The method can be used in the treatment of tumours of e.g. breast, lung, colon, kidney, bladder, head and neck, ovary, prostate or brain. The administration of a suitable antibody to

(first entry)

σ

1 QONNNWPTT

the patient makes the tumour more susceptible to radiotherapy

SXC

```
AAU77789 standard; peptide; 9 AA.
                                                                                                                                                                                      05-JUN-2002
                                                                                                                                    AAU77789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                           RESULT 3
                                                                    AAU77789
                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a method for inhibiting the growth of factactory tumours that are stimulated by a ligand of epidermal growth factor receptor (EGFR) in human patients. The method involves treating the patient with a combination of EGFR/human EGF-1 (HER1) antagonist, optionally with a chemotherapeutic agent or radiation. The antagonist can be for example a chimeric anti-EGFR monoclonal antibody, C25. The EGFR/HER1 antagonist is useful for inhibiting the growth of refractory tumours such as tumours of breast, heart, lung, small intestine, colon, spinen, kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin, bone, bone marrow, blood, thymus, uterus, testicles, cervix and liver, preferably squamous cell carcinomas. The present sequence represents the light chain variable region complementarily determining region 3 amino acid sequence of the chimeric anti-EGFR monoclonal antibody C225 which is used in an example illustrating the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epidermal growth factor receptor/human epidermal growth factor receptor-1 antagonist for inhibiting the growth of refractory tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Refractory tumour growth inhibition, epidermal growth factor receptor, BGFR antagonist, cancer, squamous cell carcinoma, anti-EGFR antibody; complementarity determining region, CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-EGFR monoclonal antibody L chain V region CDR3 peptide sequence.
                                                                                           Gaps
                                                                                           .;
0
                                        100.0%; Score 56; DB 3; Length 9; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 14; 31pp; English
                                                                                                                                                                                                                                                                                                           AAB37957 standard; protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00312284
99US-00374028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000; 2000WO-US011756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                      Query Match
Best Local Similarity 100...
                                                                                                                                           1 QONNNWPTT 9
                                                                                                                                                                                    QONNNWPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-016160/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAC83240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200069459-A1.
Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1999;
13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waksal HW;
                                                                                                                                                                                                                                                                                                                                                         AAB37957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus sp.
                                                                                                                                                                                                                                                           AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB37957
AAB3797
AAB3797
AAB3797
AAB3797
AAB3797
AAB3797
AAB3797
AAB3797
AA
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hyperproliferative disease stimulated by a ligand of a member of the epidermal growth factor (EGF) family of receptors. The method involves administering an antibody or a defective receptor that is an antagonist of a member of the EGF receptor family, or a combination of the antagonist and phototherapy. Chemotherapeutic agent or radiation therapy. The antibody used in the method of the invention acts as an epidermal phosphorylation. The method of the invention is useful for treating a mammal with hyperproliferative disease such as psoriasis, actinic strandard by a ligand of a member of the EGF family of receptor. This sequence represents the murine anti-EGF 255 antibody light chain (LH) hypervariable region (CDR3) used as an inhibitor of EGFR in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating a mammal with hyperproliferative disease especially psoriasis, stimulated by ligand of member of epidermal growth factor family of receptors, by administering antagonist of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel method for treating a mammal with
                                                            Mouse, light chain; antibody; hyperproliferative disease; epidermal growth factor; EGF; psoriasis; actinic keratosis; seborrheic keratosis; warts; keloid scars; eczema; 255 antibody; hypervariable region; CDR3; EGFR inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
Mouse light chain hypervariable region (CDR3) of 225 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 100.0%; Score 56; DB 5; Length 9; Similarity 100.0%; Pred. No. 1.40+06; 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW08949 standard; protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 12; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2000; 2000US-00635974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001; 2001WO-US041647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QUNNNNPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-257423/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QONNNWPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABK11445.
                                                                                                                                                                                                                                                                                                                              WO200211677-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention
                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Teufel T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
AAW08949
ID AAW0
```

. 0

Gaps

.,

100.0%; Score 56; DB 4; Length 9; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 9; Conservative

Query Match

1 CONNNWPTT 9

AAW08949;

domo sapiens

Key Region Region Region Region Region Region Region

```
Kappa; light chain; reshaped; monoclonāl; antibody; 225RA; human; celj; epidermal growkh factor; BGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostatic variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (MAD) H225, 225RKA. The MAD is specific for the human epidermal growth factor (EGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytocoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 56; DB 2; Length 107; 100.0%; Pred. No. 0.083; tive 0; Mismatches 0; Indels
                                                                Kappa light chain variable region of 225RA antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                     50. .56
//label= CDR_2
57. .88
//label= framework_3
89. .97
//label=_CDR_3
                                                                                                                                                                                                                                      ...23
'label= framework_1
                                                                                                                                                                                                                                                                                                                                                                                                                                      98. .107
/label= framework_4
                                                                                                                                                                                                                   location/Qualifiers
                                                                                                                                                                                                                                                                                                                     framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW08945
ID AAW08945 standard; protein; 127 AA.
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 29; Fig 21; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                   /label= CDR_1
35. .49
/label= framew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US009847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-00482982,
95US-00573289,
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCHNINAPTT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OONNNWPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldstein NI,
                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
15-DEC-1995;
                                18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-1996.
AAW08948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                      Key
Region
                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                           Kappa; light chain; reshaped; monoclonal; antibody; 225RB; human; pepidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; framework; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (MAD) H325, 225RA, The MAD is specific for the human epidermal growth factor (BGF) receptor. The MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 56; DB 2; Length 107; larity 100.0%; Pred. No. 0.083; Conservative 0; Mismatches 0; Indels
                                                           Kappa light chain variable region of 225RB antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                               35. .49
/label= framework_2
/label= CDR_2
57. .88
/label= framework_3
99. .97
/label= CDR_3
                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                   .. .23
|label= framework_1
                                                                                                                                                                                                                                                                                                                                                                                                                                      98. .107 —
/label= framework_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW08948 standard; protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 29; Fig 21; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                               CDR_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US009847,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-00482982.
95US-00573289.
                            (first entry)
                                                                                                                                                                                                                                                                     24. .34
/label= (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QONNNWPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OQNNNWPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 107 AA
```

Goldstein NI,

07-JUN-1996;

19-DEC-1996

07-JUN-1995; 15-DEC-1995;

WO9640210-A1

ö

Gaps

.. 0

RESULT 5
AAW08948
ID AAW0:

ò

- nsed

```
Kappa, light chain; reshaped; monoclonal; antibody; 225RA; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region.
                                                                                                                                                                                                                                                                                                                                                              Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the kappa light chain variable region of the murine monoclonal antibody (MAb) M225, which is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor. (Updated on 27-MUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 56; DB 2; Length 127; 100.0%; Pred. No. 0.099; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kappa light chain variable region of 225RA antibody.
                                                                                                                                                                                                                                                                  Soldstein NI, Giorgio NA, Jones ST, Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                       Example IV; Fig 13; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW08946 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                             (MRCC-) MRC COLLABORATIVE CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00482982.
95US-00573289.
                                                                                                            96WO-US009847.
                                                                                                                                                 95US-00482982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US009847
                                                                                                                                                                                                            (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity luv..
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 QQNNNNNPTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QQNNNNWPIT 9
                                                                                                                                                                                                                                                                                                         WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 correct OS field.)
                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT49338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
15-DEC-1995;
                                  WO9640210-A1.
                                                                                                              07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1996;
                                                                                                                                                 07-JUN-1995;
                                                                                                                                                                     S-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1996.
                                                                         19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW08946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW08946
ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                            Kappa; light chain; murine; mouse; monoclonal; antibody; C225; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; chimeric; L7'CL; leader sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kappa; light chain; murine; mouse; monoclonal; antibody; M225; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the kappa light chain variable region of the chimeric monoclonal antibody (MAD) C225, with the modified leader sequence from the kappa light chain of L7/CL MAD. C225 is specific for the human epidermal growth factor (EGF) receptor. C225, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage special tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric and humanised versions of anti-EGF receptor antibody 225 - used for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 56; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kappa light chain variable region of M225 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saldanha JW;
                                                                           Kappa light chain variable region of C225 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldstein NI, Giorgio NA, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example IV; Fig 17; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW08941 standard; protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                       96WO-US009847
                                                                                                                                                                                                                                                                                                                                                                                                                           95US-00482982.
                                    18-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 QONNNWPIT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QQNNNNNPTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-051897/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT49344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 127 AA;
                                                                                                                                                                                                                 Mus, spp.
Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                             WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                         1996;
                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-2003
18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                    19-DEC-1996,
    AAW08945;
                                                                                                                                                                                                                                                                          Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW08941;
```

ö

Gaps

.

ö

Gaps

à 셤

```
scrv(225) (AAW05133) comprises the single-chain binding region of murine monoclonal antibody 225, which is specific for the human epidermal growth factor receptor. It is encoded by plasmid pWW152-225 (see also AAT42033), constructed by cloning MAD 225 whand VL region CDNAs into plasmid pWM152. Novel bivalent proteins (see also AAW05134-44), some of them including scFv(225) and an effector e.g. cytotoxin, can be produced in bacterial host cells, and are useful as antitumour agents
prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bivalent fusion proteins that bind epidermal growth factor receptor canalogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                   EGF;
therapy.
                                                                                                                         ..
0
                                                                                        100.0%; Score 56; DB 2; Length 127, 100.0%; Pred. No. 0.099; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Single chain antibody; scrv; monoclonal antibody; MAb; epidermal growth factor; receptor; antitumour; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .119
/label= VH region
/label= monoclonal antibody 225 VH"
/label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "monoclonal antibody 225 VL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "synthetic spacer peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                               AAW05133 standard; protein; 240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 17; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                                                    Single chain antibody scFv(225).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Groner B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95EP-00106275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95EP-00106275.
                                                                                                                                                                                                                                                                                                                          29-JAN-1997 (first entry)
                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label=
                                                                                                                                                                                 109 QQNNNNPTT 117
                                                                                                                                                      თ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmidt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-478748/48.
                                                                                                                                                      1 QONNNWPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT42033.
                                                             Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP739984-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                Mus; sp.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                            AAW05133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wels W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                AAW05133
                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kappa; light chain; murine; mouse; monoclonal; antibody; C225; human; epidermal growth factor; EGF; receptor; inhibition; growth; tumour; cell; late stage; prostatic; prostate; variable region; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the kappa light chain variable region of the chimeric monoclonal antibody (MAD) C225, which is specific for the human epidermal growth factor (EGP) receptor. MAD, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - nsed
                                                              - nseq
                                                                                                                                    The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (WAb) H225, 225KRA, The MAb is specific for the human epidermal growth factor (EGF) receptor. The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytocoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell cycle inhibitor
                                                                                                                                                                                                                                                                                                                          Gaps
                                                           Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tumour growth, esp. of late stage prostatic tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric and humanised versions of anti-EGF receptor antibody 225 for inhibiting tummour growth, esp. of late stage prostatic tummour.
                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                          100.0%; Score 56; DB 2; Length 127; 100.0%; Pred. No. 0.099; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soldstein NI, Giorgio NA, Jones ST, Saldanha JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kappa light chain variable region of C225 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW08943 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example IV; Fig 15; 112pp; English.
                                                                                                        Claim 31; Fig 19; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMCL-) IMCLONE SYSTEMS INC. (MRCC-) MRC COLLABORATIVE CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00482982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US009847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                         Similarity 100
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    QONNWWHTT 117
                                                                                                                                                                                                                                                                                                                                                       1 QONNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-051897/05.
N-PSDB; AAT49342.
                WPI; 1997-051897/05.
N-PSDB; AAT49345.
                                                                                                                                                                                                                                                               Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spp.
sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9640210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                      109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW08943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW08943
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
```

9

ö

Gaps

.; 0

```
Query Match 100.0%; Score 56; DB 2; Length 651; Best Local Similarity 100.0%; Pred. No. 0.55; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                Mus; sp.
Pseudomonas; aeruginosa.
Synthetic.
Chimeric.
                                                                                                 269
                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wels W, Schmidt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-478748/48.
                                                                                                                                                                                                                                       scFv2 (225/FRP5) -ETA
                                                                                                  261 QONNNWPIT
                                                                         1 QONNNWPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT42040.
Sequence 651 AA;
                                                                                                                                                                                                             29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP739984-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-0CT-1996
                                                                                                                                                                                        AAW05140;
                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                        RESULT 12
                                                                                                                                                     AAW05140
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scFv(225)-ETA (AAW05135) comprises the single-chain binding region (see also AAW05133) of murine monoclonal antibody 225, which is specific for human epidermal growth factor receptor, joined to extoxin A (ETA). It is encoded by plasmid pSW020-225 (see also AAT42035) obtd. by ligating an scFv(225) gene (AAT42033) into plasmid pSW200 contg. the Pseudomonas eruginose PAK ETA gene. The construct can be used to produce novel bivalent fusion proteins (see also AAW05136-44) in bacterial host cells, for use as antitumour agents
                                                                                                                                                                                                                                                   Single chain antibody; scFv; monoclonal antibody; MAb; EGF; epidermal growth factor; receptor; plasmid pSW202-225; cancer; therapy; antitumour; exotoxin A; ETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bivalent fusion proteins that bind epidermal growth factor receptor analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                     ;
0
         'Match 100.0%; Score 56; DB 2; Length 240; Local Similarity 100.0%; Pred. No. 0.19; es 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "exotoxin A amino acids 252-613"
                                                                                                                                                                                                                                                                                                                                                                               1. .21
/label= Sig_peptide
/note= "ompA signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; Page 19-20; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                 AAW05135 standard; protein; 651 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                  22. .38
/label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279. .289
/label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Groner B;
                                                                                                                                                                                                                           scFv(225)-ETA fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95EP-00106275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95EP-00106275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290. .651
/label= ETA
                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                    Mus sp.
Pseudomonas; aeruginosa.
                                                                             223 QONNNWPTT 231
                                                             1 QONNNWPIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schmidt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-478748/48
N-PSDB; AAT42035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-APR-1995;
                                                                                                                                                                                                 29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP739984-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-0CT-1996
                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                           AAW05135;
                                                                                                                                                                                                                                                                                                                                           Chimeric.
            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wels W,
                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                         Best Loca
Matches
                                                                                                                        g
                                                              ਨੇ
```

```
Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                   Single chain antibody; scFv; monoclonal antibody; MAb; EGF; erbB-2; epidermal growth factor; receptor; plasmid pMS238-225-5; cancer; exotoxin A; ETA; antitumour.
                                                                                                                                                                                                                                                                                                                                            /note= "endotoxin-A amino acids 380-613"
                                                                                                                                                                                                                                           90. .404⁻
|abel= ETA
'note= "exotoxin A amino acids 252-366"
                                                                                                                                                             . .21
|abel= Sig_peptide
note= "ompA signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 11; Page 31-33; 52pp; English.
                                                                                                                                                    iocation/Qualifiers
AAW05140 standard; protein; 892 AA.
                                                                                                                                                                                                                                                                                                SCFV (FRP5)
                                                                                                                                                                                                        9. .278
label= scFv(225)
                                                                                                                                                                                                                                                                                                                                                                                                                                    (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                 /label= Spacer
659. .892
/label= ETA
                                                                                                                                                                                                                                                                     405. .407
/label= Spacer
408. .647
/label= scFv(FR)
                                                                                                                                                                                      2. .38
label= Spacer
                                                                                                                                                                                                                         79. .289
label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Groner B;
                                                                                                                                                                                                                                                                                                                                                                                                95EP-00106275
                                                                                                                                                                                                                                                                                                        648. .658
/label= Sp.
                                   (first entry)
```

Groner B;

Schmidt M,

```
scrv2(225/FRP5)-STA (AAW05140) comprises the single-chain binding region of murine monoclonal antibody 225 (specific for human epidermal growth actor receptor, see also AAW0513) joined to portions of exotoxin A from Pseudomonas aeruginosa and to the single-chain binding region of murine monoclonal antibody FRP5 (specific for human epidermal growth factor receptor erbB-2, see also AAW05134). It is encoded by plasmid pMS28-225-5 (AAT42040). This plasmid can be utilised in the prodn. Of the bivalent fusion protein in bacterial (egg. E. coli) host cells. Such fusion proteins (see also AAW05138-44) are useful as antitumour agents
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Single chain antibody; scFv; monoclonal antibody; MAb; EGF; erbB-2; epidermal growth factor; receptor; plasmid pMS238-5-225; cancer; exotoxin A; ETA; antitumour.
                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Jabel = Spacer

/ Jabel = ScFv(FRP5)

/ Jabel = Spacer

290. .404

/ Jabel = ETA

/ Jabel = ETA

/ Jabel = Spacer

405. .407

/ Jabel = ScFv(225)

648. .658

/ Jabel = Spacer

/ Jabel = Spacer

659. .892

/ Jabel = Spacer

659. .892

/ Jabel = ETA

/ Jabel = Spacer

659. .892

/ Jabel = ETA

/ Jabel = ETA
                                                                                                                                                           100.0%; Score 56; DB 2; Length 892;
100.0%; Pred. No. 0.76;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .21
|label= Sig_peptide
|/note= "ompA signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                  AAW05139 standard; protein; 892 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SANT-) SAN TUMORFORSCHUNGS GMBH
                                                                                                                                                                                                                                                                                                                                                                           scFv2(FRP5/225)-ETA (version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22. .38
/label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95EP-00106275
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus; sp.
Pseudomonas; aeruginosa.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                  261 QONNNWPTT 269
                                                                                                                                                                                                              σ
                                                                                                                                                                                                            1 QONNNWPTT
                                                                                                                                     Seguence 892 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                   29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP739984-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-0CT-1996
                                                                                                                                                                                                                                                                                                                           AAW05139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                    g
X88888888888X8
```

```
·.
                                                                                                                                                                                                                                                                                                         scFv2(FRP5/225)-ETA (AAW05139) comprises the single-chain binding region of murine monoclonal antibody FRP5 (specific for human epidermal growth factor receptor exbB-2, see also AAW05134) joined to portions of exotoxin A from Pseudomonas aeruginosa and to the single-chain binding region of murine monoclonal antibody 225 (specific for human epidermal growth factor receptor, see also AAW05131). It is encoded by plasmid pMS238-5-225 (AAT42039). This plasmid can be utilised in the prodn. of the bivalent fusion protein in bacterial (sep. E. coli) host cells. Such fusion proteins (see also AAW05138-44) are useful as antitumour agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                 Bivalent fusion proteins that bind epidermal growth factor receptor analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single chain antibody, scFv; monoclonal antibody; MAb; EGF; erbB-2; epidermal growth factor; receptor; plasmid pMS240-5-225; cancer; exotoxin A; ETA; antitumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 100.0%; Score 56; DB 2; Length 892; Local Similarity 100.0%; Pred. No. 0.76; nes 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acids 252-366"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .21
/label= Sig_peptide
/note= "ompA signal peptide"
                                                                                                                                                                                                                                                                 Example 11; Page 28-30; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW05141 standard; protein; 1020 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22. .38
/label= Spacer
39. .278
/label= scFv (FRP5)
279. .289
/label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Spacer
408. 647
/label= scFv(225)
648. 658
/label= Spacer
659. 1020
/label= ETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "exotoxin
05. .407
label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scFv2(FRP5/225)-ETA (version 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90. .404
| label = ETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus; sp.
Pseudomonas; aeruginosa.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                          WPI; 1996-478748/48.
N-PSDB; AAT42039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QONNNWPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           630 QONNWPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 892 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW05141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric
                      Wels W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW05141
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE LITTLE LITTL
```

Kaluza B, Riethmueller G;

91DE-04143214. 91DE-04124759.

```
This sequence is the light chain variable region of a preferred anti-IL2R beta monocolonal antibody for use in the claimed synergistic composition. The anti-IL2R beta antibody is used with at least one anti-CD4 antibody. Individually the antibodies are strongly inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response. See AAQ36607-Q36616. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                               Synergistic antibody compsn. for use as immunosuppressant - comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-
                                                                                                                                       (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 17; 18pp; German.
                                                                                                                                                                                                         Scheuer W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LL2R beta antibodies.
                                                                                                                                                                                                                                                                               WPI; 1993-037582/05.
                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ36615
   30-DEC-1991;
                                                                  25-JUL-1991;
                                                                                                                                                                                                             Weidle U,
   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scFv2(FRPS/225)-ETA version 2 (AAW05141) comprises the single-chain binding region of murine monoclonal antibody FRPS (specific for human epidermal growth factor receptor exbB-2, see also AAW05134) joined to portions of exotoxin A from Pseudomonas aeruginosa and to the single-chain binding region of murine monoclonal antibody 225 (specific for human epidermal growth factor receptor, see also AAW05131). It is encoded by plasmid pMS246-5-225 (AAT40511). This plasmid can be utilised in the profin of the bivalent fusion protein in bacterial (ssp. E. coli) host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bivalent fusion proteins that bind epidermal growth factor receptor or analogues - and comprise at least two different cell surface binding domain(s), useful for tumour therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prodn. of the bivalent fusion protein in bacterial (esp. E. coll, cells. Such fusion proteins (see also AAW05138-44) are useful as antitumour agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 100.0%; Score 56; DB 2; Length 1020; Local Similarity 100.0%; Pred. No. 0.88; No. 0.88; No. 0.88; No. 0, Indels (
   /note= "endotoxin-A amino acids 252-613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 11; Page 34-36; 52pp; English.
                                                                                                                                                                                                                                                                                                                                              (SANT-) SAN TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                   Groner B;
                                                                                                                                                                                                                                                                            95EP-00106275.
                                                                                                                                                                                                      95EP-00106275
                                                                                                                                                                                                                                                                                                                                                                                                                   Schmidt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-478748/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT42041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1020 AA;
                                                                                                                                                                                                      26-APR-1995;
                                                                                                                                                                                                                                                                            26-APR-1995;
                                                                                                                                       30-OCT-1996,
                                                                  EP739984-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Si
Matches 9;
                                                                                                                                                                                                                                                                                                                                                                                                            Wels W,
NAME OF THE PROPERTY OF THE PR
```

```
o;
                                               Gaps
                                               ..
0
                       Length 107;
                                              1; Indels
                    80.4%; Score 45; DB 2; 77.8%; Pred. No. 5.6; iive 1; Mismatches
                                                                                                                                   6, 2004, 16:29:50
           Query Match
Best Local Similarity 77.0
Best Local 7; Conservative
                                                                                            97
                                                                                                                             Search completed: October
Job time: 47.4737 secs
                                                                      0
                                                                      1 OQNNNWPTT
                                                                                             89 QOTNSWPTT
Sequence 107 AA;
```

immunosuppression; tissue transplantation; graft; L chain; V region; T-helper cell inhibition; transplant rejection; MAb; interleukin-2 receptor.

Location/Qualifiers

Homo sapiens

Region Region

1. .96 /label= V-region 97. .107 /label= J-region

DE4143214-A1

28-JAN-1993.

Anti-IL2R beta antibody MAb A41 light chain variable region.

(first entry)

(revised) (revised)

25-MAR-2003

AAR32129;

10-MAR-2003 02-JUN-1993

AAR32129 standard; protein; 107 AA.

RESULT 15 AAR32129

630 QONNNWPTT 638

1 QONNNWPTT 9

ઠે